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RESULT 9

US-08-988-819-4
; Sequence 4, Application US/08988819
; Patent No. 6054294
GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,819
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
FEATURE:
; NAME/KEY: CDS
; LOCATION: 95..769
; FEATURE: mat_peptide
; NAME/KEY: 176..769
; CLASSIFICATION:

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; NAME/KEY: sig_peptide
; LOCATION: 95..175
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Query Match 8.4%; Score 429.6; DB 3; Length 819;
Best Local Similarity 90.4%; Pred. No. 7.9e-101; Indels 0; Gaps 0;
Matches 459; Conservative 0; Mismatches 49;
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RESULT 10

US-09-016-534-4
; Sequence 4, Application US/09016534
; Patent No. 6143874
GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: ELLIOTT, GARY S.
; APPLICANT: SARMIENTO, ULLA
; APPLICANT: SENALDI, GIORGIO
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,534
; FILING DATE:
; CLASSIFICATION:

Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)583-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
US-08-232-463-14

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Best Local Similarity 5.1%; Pred.No. 4.2e-15;
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RESULT 13

US-09-249-585A-4
Sequence 4, Application US/09249585A
Patent No. 6417002
GENERAL INFORMATION:
APPLICANT: Horlick, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISODES
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1926
TYPE: DNA
ORGANISM: Epstein Barr Virus
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(1926)
OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

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Best Local Similarity 46.6%; Pred.No. 2.1e-05;
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DB 401 CT 460
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QY 2935 GCTGAGGCTGTCT 2994
DB 521 CCGTCT 580
QY 2995 CT 3054
DB 581 CT 639
QY 3055 ACTC---TCCCAAGGTTTCCCAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3110

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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	819	100.0	819	10	AF176913	AF176913 Mus muscu
5	674	82.3	881	6	AX205024	AX205024 Sequence
6	674	82.3	881	6	AX205042	AX205042 Sequence
7	669.4	81.7	797	6	AR002595	AR002595 Sequence
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18	507.2	61.9	258710	2	AC135823	AC135823 Rattus no
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DEFINITION	Sequence 4 from patent US 5741772.					
ACCESSION	AR002597					
VERSION	AR002597.1	GI:3964151				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 819)					
AUTHORS	Chang, M.-s.					
TITLE	Neurotrophic factor NNT-1					
JOURNAL	Patent: US 5741772-A 4 21-APR-1998;					
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DEFINITION Sequence 4 from Patent WO0215977.
ACCESSION AX392089
VERSION    AX392089.1 GI:19700577
KEYWORDS

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SOURCE          Mus sp.
ORGANISM        Mus sp.
REFERENCE        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE            Senaldi, G.
JOURNAL          Methods and compositions for treating ige-related disease using mn
FEATURES         t-1 inhibitors
SOURCE           Patent: WO 0215977-A 4 28-FEB-2002;
                  Angen Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 9.8e-179; Indels 0; Gaps 0;
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ORIGIN
Query Match      100.0%; Score 819; DB 10; Length 819;
Best Local Similarity 100.0%; Pred. No. 9.8e-179;
Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GGGATGTTAGCTTGCCTATGACGCTGTGTGGACCTCCCTGCGAGTCCAGCTCTTAA 180
DB 121 GGGATGTTAGCTTGCCTATGACGCTGTGTGGACCTCCCTGCGAGTCCAGCTCTTAA 180

QY 181 TCGCAGAGAGATCCAGGCGCTGGCGCTCCATCCAGAAAACCTATGACCTCACCGGTA 240
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QY 241 CTGAGAGATCAACTCCGAGCTTGTAGTGGGACCTTACCTGAACTACTGCGGCGCGCTTT 300
DB 241 CTGAGAGATCAACTCCGAGCTTGTAGTGGGACCTTACCTGAACTACTGCGGCGCGCTTT 300

QY 301 CAACGAGCTGACTTCAATCTCTCGACTGGGCGCAGAACTCTGCCAGGCGCGCGCT 360
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QY 361 CAATTTGGAAGTGTGGCGAAGCTCAATGACAGGCTGGCGCTGACCCAGAACTATGAGGC 420
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QY 421 GTACAGTCACTCTCTGTGTACTTGGTGGCTCAACGCTCAGGCTGCCAGCTGAACT 480
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QY 781 CCTTAACCCCACTCCAGGCGCGCGCTGCTGCTT 819
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DB 781 CCTTAACCCCACTCCAGGCGCGCGCTGCTGCTT 819

RESULT 5
AX205024
LOCUS      AX205024
DEFINITION Sequence 1 from Patent WO0155172.
ACCESSION AX205024
VERSION    AX205024.1 GI:15394259
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS    Elson,G., Gauchat,J.F., Plun-Pavreau,H., Chevalier,S. and Gascan,H.
TITLE       Isolated complex comprising a nnt-1 protein and in addition at
            least a clf-1 protein and/or a scntfr_g(a) protein
JOURNAL     Patent: WO 0155172-A 1 02-AUG-2001;
            PIERRE FABRE MEDICAMENT (FR); INSTITUT NATIONAL DE LA SANTE ET DE
            LA RECHERCHE MEDICALE (INSERM) (FR)
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ORIGIN
Query Match      82.3%; Score 674; DB 6; Length 881;
Best Local Similarity 92.2%; Pred. No. 3.1e-145;
Matches 721; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

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DB 82 ATTATTAAGCTTCGCGAGCGCGGCTCGCCCTCCCACTCCGCGAGCTCTGGGAGA 141

QY 62 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 121
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DB 201 GGGATGTTAGCTTGCCTATGACGCTGTGTGGACCTCCCTGCGAGTCCAGCTCTTAA 260

QY 182 CGCAGAGAGATCCAGGCGCTGGCGCTTCATCAGAAAACCTATGACCTCACCGCTAC 241
DB 261 CGCAGAGAGATCCAGGCGCTGGCGCTTCATCAGAAAACCTATGACCTCACCGCTAC 320

QY 242 CTGAGAGATCAACTCCGAGCTTAGCTGGGACCTACTGAACTACTGCGGCGCGCTTTC 301
DB 321 CTGAGAGATCAACTCCGAGCTTAGCTGGGACCTACTGAACTACTGCGGCGCGCTTTC 380

QY 302 AACGAGCTGACTTCACTCTCTCTGACTGGGCGGAGAACTCTGCCAGGCGCGAGGTC 361
DB 381 AACGAGCTGACTTCACTCTCTCTGACTGGGCGGAGAACTCTGCCAGGCGCGAGGTC 440

QY 362 AACTTGAAGTGTGGGGAAGCTCAATGACAGCTCGGCTCACCCAGAACTATGAGGCG 421
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681 ACTCCTGGCCCTGCCCACTGAGTACTTCTCCAGAGATGAGTACTTCTGGCTGCTGAAG 740
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722 CAGCCTCCAGAGCTTCAAGTCAACCTGACCTGAGGACATGTTTCTGACCTCTGACC 781
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782 CT 783
861 TT 862

RESULT 6
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LOCUS AX205042 881 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 1 from Patent WO0155219.
ACCESSION AX205042
VERSION AX205042.1 GI:15394277
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Elson,G. and Gauchat,J.F.
TITLE Secentr/nnt-1 fusion protein
JOURNAL Patent: WO 0155219-A 1 02-AUG-2001;
PIERRE FABRE MEDICAMENT (FR)
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ORIGIN
Query Match 82.3%; Score 674; DB 6; Length 881;
Best Local Similarity 92.2%; Pred. No. 3.1e-145;
Matches 721; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

QY 2 ATTATTAAGCTTCGCGAGCCGCGCTCGCCCTCCCACTCCCGCAGCTCTGGGAGAG 61
DB 82 ATTATTAAGCTTCGCGAGCCGCGCTCGCCCTCCCACTCCCGCAGCTTCGCGGAGAG 141
QY 62 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 121
DB 142 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 200
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182 CGCACAGGAGATCCAGGGCCCTGGCCCTCCATCCAGAAAAACCTATGACTCACCGCTAC 241
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441 GACTTTGGAGGTGTGGGAGAGCTCAATGACAACTGGCGCTGACCCAGAACTACGAGGCC 500
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501 TACAGCCACTTCTGTGTTACTTGTGGCTCAACCGTCAAGCTCAGGCTGCCACTGCTGAGCTG 560
482 CGAGCTAGCCTGGCCCACTTCTGTACAGCCTCCAGGGCTGCTGGGCGAGCATTTGAGGT 541
561 CGCGCAGCCTGGCCCACTTCTGTCAACAGCCTCCAGGGCTGCTGGGCGAGCATTTGCGGC 620
542 GTCATGGGAGCCTTGGGTACCCACTGCCAGGCTCTGCCAGGGACTGAGCCAGCTGG 601
621 GTCATGGGAGCCTTGGGTACCCACTGCCAGGCTGCTGGGCGAGCTGAGCCAGCTGG 680
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782 CT 783
861 TT 862

RESULT 7
AR002595
LOCUS AR002595 797 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 1 from patent US 5741772.
ACCESSION AR002595
VERSION AR002595.1 GI:3964149
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 797)
AUTHORS Chang,M.-s.
TITLE Neurotrophic factor NNT-1
JOURNAL Patent: US 5741772-A 1 21-APR-1998;
FEATURES Location/Qualifiers
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Query Match 81.7%; Score 669.4; DB 6; Length 797;
Best Local Similarity 92.0%; Pred. No. 3.6e-144;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
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LOCUS AX392086 797 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 1 from Patent WO0215977.
ACCESSION AX392086
VERSION AX392086.1 GI:19700574
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Senaldi, G.
TITLE Methods and compositions for treating ige-related disease using nn
t-1 inhibitors
JOURNAL Patent: WO 0215977-A 1 28-FEB-2002;
Amgen Inc. (US)
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ORIGIN

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Query Match 81.7%; Score 669.4; DB 6; Length 797;
Best Local Similarity 92.0%; Pred. No. 3.6e-144;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
QY 5 ATTAAGCTTCGCGGAGCGGGCTCGCCCTCCACCTCCGCGAGCGCTCTGGGAGGAG 64
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QY 665 CTGCAGACTTGGCTATGGGCTTACCGAGGACTTCAACCGCTTCAACCGCTTCAACCGCT 724
Db 660 CTGCAGACTTGGCTATGGGCTTACCGAGGACTTCAACCGCTTCAACCGCTTCAACCGCT 719
QY 725 CTCCAGCAGCTTCACTGACCTTGCATCTGGGAGCAGATGTTTCTGACCTTCAACCTT 783
Db 720 CTCCAGCAGCTTCACTGACCTTGCATCTGGGAGCAGATGTTTCTGACCTTCAACCTT 778

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RESULT 9
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LOCUS The neurotrophic factor NNT-1.
ACCESSION BD195447
VERSION BD195447.1 GI:33005217
KEYWORDS JP 2002514067-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 797)
AUTHORS Chang,M.S., Elliott,G.S., Senaldi,G. and Sarmiento,U.
TITLE The neurotrophic factor NNT-1
JOURNAL Patent: JP 2002514067-A 1 14-MAY-2002;
AMGEN INC
COMMENT OS Unidentified
PN JP 2002514067-A/1
PD 14-MAY-2002
PF 02-FEB-1998 JP 1998533258
PR 03-FEB-1997 US 08/792019,30-JAN-1998 US 09/016534 PT
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Strandedness: Single;
CC Topology: Linear;
CC The neurotrophic factor NNT-1
FH Key Location/Qualifiers
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FT mat peptide 171..764
FT sig peptide 90..170.
FT Location/Qualifiers
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FEATURES
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Query Match 81.7%; Score 669.4; DB 6; Length 797;
Best Local Similarity 92.0%; Pred. No. 3.6e-144;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
QY 5 ATTAAGGCTTCGCGGAGCGCGCTCGCCCTCCACTCCGCGCAGCTCTGGGAGGAG 64
DB 1 ATTAAGGCTTCGCGGAGCGCGCTCGCCCTCCACTCCGCGCAGCTCTGGGAGGAG 60
QY 65 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 124
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LOCUS Homo sapiens neurotrophin-1/B-cell stimulating factor-3 mRNA,
DEFINITION complete cds.
ACCESSION AF176911
VERSION AF176911.1 GI:6007640
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 797)
AUTHORS Senaldi,G., Varnum,B.C., Sarmiento,U., Starnes,C., Lile,J.,
Scully,S., Guo,J., Elliott,G., McNinch,J., Shaklee,C.I.,
Freeman,D., Manu,F., Simonet,W.S., Boone,T. and Chang,M.S.
Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the
IL-6 family
Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11458-11463 (1999)
99432254
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2 (bases 1 to 797)
Senaldi,G., Varnum,B., Sarmiento,U., Lile,J., Starnes,C.,
Scully,S., Guo,J., Elliott,G., McNinch,J., Freeman,D., Shaklee,C.,
Manu,F., Simonet,S., Boone,T. and Chang,M.S.
Direct Submission
Submitted (11-AUG-1999) Amgen, Inc., One Amgen Center Drive,
Thousand Oaks, CA 91320, USA
Location/Qualifiers
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CDS
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Best Local Similarity 92.0%; Pred. No. 3.6e-144;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
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QY 125 ATGTAGCTTCGCTATGACGCTGCTGCGACCTCCCTGCGAGTCCGAGCTCTAATCG 184
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QY 305 GAGCTGACTTCAATCTCTCTGACTGGGCGAGAACTCTGCCAGGCGCGCGCTCAAC 364
DB 300 GAGCCAGACTTCAACCTCTCCCGCTGGGCGAGAGACTCTGCCAGGCGCGCTGTGAC 359
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Tue Aug 17 06:05:00 2004

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QY	816	GCTT 819	
Db	22429	GCTT 22432	

Search completed: August 15, 2004, 23:47:35
Job time : 3064.2 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 15:26:00 ; Search time 1864.29 Seconds
(without alignments)
13118.770 Million cell updates/sec

Title: US-09-931-704-4
Perfect score: 819
Sequence: 1 tattattaaagcttcgcgg.....aggccacgtcagctgtgctt 819

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_man.*
23: em_gss_mus.*
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27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	671.4	82.0	678	13	BY735168
2	660.4	80.6	662	29	AY409172
3	644.4	78.7	887	13	BQ948158
4	601.2	73.4	788	14	CF271927

5	600.8	73.4	804	14	CF271929
6	599	73.1	787	14	CK130210
7	598.6	73.1	752	14	CF271925
8	596	72.8	810	14	CK130212
9	590.2	72.1	806	14	CK130211
10	572.4	69.9	862	29	AY409170
11	572.4	69.9	862	29	AY409171
12	568.6	66.4	1157	13	BQ940483
13	544	66.4	1053	12	BG164929
14	543	66.3	853	12	BG437538
15	541	66.1	800	14	CF271926
16	504.6	61.6	594	12	BM763333
17	502	61.3	801	14	CF271930
18	499.2	61.0	763	14	CF271924
19	491.2	60.0	580	12	BM848189
20	485.2	59.2	573	12	BM840863
21	476	58.1	476	10	BE632644
22	473.4	57.8	1028	9	AL543945
23	468.2	57.2	634	13	EX497225
24	455.4	55.6	532	12	BM846370
25	448	54.7	448	13	BY531444
26	447	54.6	522	12	BM841897
27	445	54.3	542	12	BM821005
28	442.8	54.1	793	14	CK032835
29	441.4	53.9	529	12	BM847924
30	414	50.5	831	28	CC138171
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32	390.4	47.7	505	13	EX528877
33	381.4	46.6	388	13	BY022718
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36	351.2	42.9	420	12	BM764238
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39	329.8	40.3	482	12	BM846622
40	312.4	38.1	407	9	AI752561
41	295.8	36.1	392	13	BY012378
42	292.4	35.7	766	14	CF271928
43	278.4	34.0	663	13	BY722568
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ALIGNMENTS

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LOCUS
DEFINITION
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Jyg-MC(B) cDNA Mus musculus CDNA clone G930015G22 5', mRNA
678 bp mRNA linear EST 17-DEC-2002
sequence.
ACCESSION
BY735168
VERSION
BY735168.1 GI:27148295
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 678)
Oikarinen, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamashita, T.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Buit, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Cherlow, C., Corbani, L.E., Cousins, S., Della, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Matches 661; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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5', mRNA sequence.
ACCESSION BQ948158
VERSION BQ948158.1 GI:22363636

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 887)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2614 row: h column: 07
High quality sequence stop: 674.
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ORIGIN
Query Match 78.7%; Score 644.4; DB 13; Length 887;
Best Local Similarity 92.3%; Pred. No. 2.8e-133;
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Db 65 GAGCG 123
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QY 242 CTGAGAGATCACTCCGAGCTTAGCTGGGACCTACCTGAACCTACCTGGGGCCCCCTTC 301
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QY 302 AACGAGCTGACTTCAATCTCTTCGAC - TGGGGGCGAGAACTCTGCCAGGGCCACGGT 360
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 Db 664 GGAGCTGAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
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RESULT 4

CF271927

LOCUS

AGENCOURT 15196974 NIH_MGC_195 Homo sapiens cDNA clone
 IMAGE:7002180 5', mRNA sequence.

CF271927

ACCESSION

VERSION

KEYWORDS.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Aug 12, 2003 this sequence version replaced gi:33627839.
 Contact: Daniela S. Gerhardt, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 DNA Sequencing by: The I.M.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 High quality sequence stop: 761.
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 loxP-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/clontech and Washington University).
 PCR products are directionally cloned into the loxP sites

FEATURES

source

of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.4%; Score 601.2; DB 14; Length 788;
 Best Local Similarity 91.6%; Pred No 1.2e-123;
 Matches 636; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
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RESULT 5

CF271929

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CF271929 804 bp mRNA linear EST 26-NOV-2003
 AGENCOURT 15196942 NIH_MGC_195 Homo sapiens cDNA clone
 IMAGE:7002179 5', mRNA sequence.
 CF271929
 CF271929.2 GI:38558835
 Homo sapiens (human)
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

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NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

On Aug 12, 2003 this sequence version replaced gi:33627841.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: IRBK4 row: e column: 09

High quality sequence start: 13

High quality sequence stop: 711.

FEATURES

source

1..804

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loxP-HindIII; Clones from this library have been

PCR-amplified using gene-specific primers to contain the

complete open reading frame (based on known gene sequences

available from NCBI's RefSeq). Template for PCR is cDNA

derived from either pooled cytoplasmic polyA RNA from 30

cells lines or pooled total RNA from 10 different tissues

(from BD Biosciences/Clontech and Washington University).

PCR products are directionally cloned into the loxp sites

of the pDNR-Dual vector. Library constructed by Dr.

Narayan Bhat, Earl Bere III and Hongling Liao (Gene

Expression Laboratory, Research Technology Program, SAIC

Frederick, NCI-Frederick, Frederick, MD 21702). For

information on which gene each clone represents, please

visit our anonymous ftp site at

ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat

a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.4%; Score 600.8; DB 14; Length 804;

Best Local Similarity 90.4%; Pred. No. 1.4e-123;

Matches 641; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

90 GCGCCATGGAACCTCGAGCAGGGGACTCGTGGGGATGTTAGCTTGCTATGACGCTGC 149

33 GCGCCATGGAACCTCGAGCAGGGGACTCGTGGGGATGTTAGCTTGCTATGACGCTGC 92

150 TGTGGCCTCCCTGCGAGTGCCAGCTCTTAATCCACAGAGATCCAGGCCCTGGCCCT 209

93 TGTGGCCTCCCTGCGAGTGCCAGCTCTTAATCCACAGAGATCCAGGCCCTGGCCCT 152

210 CCATCCAGAAACCTATGACCTCACCGCTACCTGGAGCATCAACTCCGAGCTTAGCTG 269

153 CCATCCAGAAACCTATGACCTCACCGCTACCTGGAGCATCAACTCCGAGCTTAGCTG 212

270 GGACTACTGAACTACTCGGGGCCCCCTTTCAACAGAGCTTCAATCCCTCTCGAC 329

213 GGACTACTGAACTACTCGGGGCCCCCTTTCAACAGAGCTTCAATCCCTCTCGAC 272

330 TGGGGCAGAACTCTGCCAGGGCCAGGTCACCTTGGAGTGGCGAGCTCAATG 389

273 TGGGGCAGAACTCTGCCAGGGCCAGGTCACCTTGGAGTGGCGAGCTCAATG 332

QY 390 ACAGSGCTGGGTGACCCAGAACTATGAGCGTACAGTCACTCTCTGTGTACTTGCGTG 449

DB 333 ACRAACTGGGCTGACCCAGAACTACGAGGCTACAGCCACTTCTGTGTACTTGCGTG 392

QY 450 GCGTCAACCGTACGCTGCCACAGCTGAACCTCCGACGTAGCTGGCCCACTTCTTACCA 509

DB 393 GCGTCAACCGTACGCTGCCACAGCTGAACCTCCGACGTAGCTGGCCCACTTCTTACCA 452

QY 510 GCGTCCAGGCGCTGCTGGGCGAGCATTCGAGGTGTCATGGCGAGCGTTCGCTACCCACTGC 569

DB 453 GCGTCCAGGCGCTGCTGGGCGAGCATTCGAGGTGTCATGGCGAGCGTTCGCTACCCACTGC 512

QY 570 CCCAGCCTCTGCCAGGAGCTGAGCCAGCGCTGGGCCCCCTGGCCCTCCACAGTACTTCC 629

DB 513 CCCAGCCTCTGCCAGGAGCTGAGCCAGCGCTGGGCCCCCTGGCCCTCCACAGTACTTCC 572

QY 630 TCCAGAAGATGATGACTTCTGGCTGCTGAAGAGCTGCAGACCTGGCTATGGGCTTCAG 689

DB 573 TCCAGAAGATGATGACTTCTGGCTGCTGAAGAGCTGCAGACCTGGCTATGGGCTTCAG 632

QY 690 CCAAGGACTTCAACCGGCTTAAGAAAGATGCAGCCTCCAGAGCTTCAAGTCAACCTGC 749

DB 633 CCAAGGACTTCAACCGGCTTAAGAAAGATGCAGCCTCCAGAGCTTCAAGTCAACCTGC 692

QY 750 ACTTGAGGAGCATGGTTTCTGACCTCTGACCCCTTAACCCCCACACTC 798

DB 693 ACCTGGGGCTCATGGCTTCTGACTTCTGACTTCTCTCTTCTGCTCCNC 741

RESULT 6

CK130210

LOCUS

DEFINITION

AGENCOURT_15196910 NIH_MGC_195 Homo sapiens cDNA clone

IMAGE:7002178 5', mRNA sequence.

CK130210

ACCESSION

VERSION

CK130210.1 GI:38622146

KEYWORDS

EST.

787 bp mRNA linear EST 02-DEC-2003

1 (bases 1 to 787)

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence stop: 715.

Location/Qualifiers

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/organism="Homo sapiens"

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/db_xref="taxon:9606"

/clone="IMAGE:7002178"

/tissue_type="mixed"

/lab_host="DH5A (T1 phage-resistant)"

/clone_lib="NIH_MGC_195"

/note="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2:

loxP-HindIII; Clones from this library have been

PCR-amplified using gene-specific primers to contain the

complete open reading frame (based on known gene sequences

available from NCBI's RefSeq). Template for PCR is cDNA

derived from either pooled cytoplasmic polyA RNA from 30

cells lines or pooled total RNA from 10 different tissues

(from BD Biosciences/Clontech and Washington University).

available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.1%; Score 599; DB 14; Length 787;
 Best Local Similarity 91.4%; Pred. No. 3.6e-123;
 Matches 635; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 89 AGCCCATGAGCTCCGACGAGGACTCGTGGGGATGTAGCTTGCTATGACGGTG 148
 Db 1 AGCCCATGAGCTCCGACGAGGACTCGTGGGGATGTAGCTTGCTATGACGGTG 60

QY 149 CTGTGGCACTCCCTGAGTGCAGCTCTTATCGCAGAGAGATCCAGGCCCTGGCCCC 208
 Db 61 CTGTGGCACTCCCTGAGTGCAGCTCTTATCGCAGAGAGATCCAGGCCCTGGCCCC 120

QY 209 TCCATCCAGAAACCTATGACCTCAACCCGCTACCTGGAGCATCACTCCGAGCTTAGCT 268
 Db 121 TCCATCCAGAAACCTATGACCTCAACCCGCTACCTGGAGCATCACTCCGAGCTTAGCT 180

QY 269 GGGACCTACTGAATACCTGCGGGCCCTTTTCACAGAGCTGACTTCAATCTCTCTCGA 328
 Db 181 GGGACCTACTGAATACCTGCGGGCCCTTTTCACAGAGCTGACTTCAATCTCTCTCGC 240

QY 329 CTGGGGGAGAACTCTGCCAGGGCCAGCTCACTTGGAGTGGAGAGCTCAAT 388
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QY 389 GACAGCTCGGCTGACCCAGAACTATGAGGGGTACAGTCACTCTCTGTACTTGCGT 448
 Db 301 GACAAACTCGGCTGACCCAGAACTATGAGGGGTACAGTCACTCTCTGTACTTGCGT 360

QY 449 GGCCTCAACCTGAGCTGCGACAGTCACTCCAGTACGCTGGCCCTTCTGAC 508
 Db 361 GGCCTCAACCTGAGCTGCGACAGTCACTCCAGTACGCTGGCCCTTCTGAC 420

QY 509 AGCCTCCAGGGCTGCTGGGACAGCTTGCAGGTGTATGGGACCGCTTGGCTACCCACTG 568
 Db 421 AGCCTCCAGGGCTGCTGGGACAGCTTGCAGGTGTATGGGACCGCTTGGCTACCCACTG 480

QY 569 CCGCAGCTCTGCGAGGAGTACGAGCTGGGCGCTTGGCCCTGCGCCACAGTACTTC 628
 Db 481 CCGCAGCTCTGCGAGGAGTACGAGCTGGGCGCTTGGCCCTGCGCCACAGTACTTC 540

QY 629 CTCAGAGATGATGACTTCTGGTGTGAGAGAGCTGCGAGCTGCTATGGCGTTCA 688
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QY 689 GCGAAGGACTTCAACCGGCTTAAGAGAGATGACAGCTCCAGAGCTTCAAGTCAACCGTG 748
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QY 749 CACTTGGAGGACATGTTTCTGACTCTGACCT 783
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RESULT 7

CF271925

LOCUS

DEFINITION

CF271925 752 bp mRNA linear EST 26-NOV-2003
 AGENCOURT 15197006 NIH_MGC 195 Homo sapiens cDNA clone
 IMAGE:7002181 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF271925
 CF271925.2 GI:38558833

EST.
 Homo sapiens (human)

Homo sapiens

Eukaryota; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgs.nci.nih.gov/

1 (bases 1 to 752)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

On Aug 12, 2003 this sequence version replaced gi:33627837.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: c9apbs-f@mail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRBK4 row: e column: 11

High quality sequence stop: 743.

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:7002181"

/tissue_type="mixed"

/lab_host="DH5A (T1 phage-resistant)"

/note="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2: loxp-HindIII; clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat a Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 73.1%; Score 598.6; DB 14; Length 752;
 Best Local Similarity 90.3%; Pred. No. 4.3e-123;
 Matches 640; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 90 GCCCATGAGCTCCGACGAGGACTCGTGGGGATGTAGCTTGCTATGACGGTG 149
 Db 6 GCCCATGAGCTCCGACGAGGAGCTCGTGGGGATGTAGCTTGCTATGACGGTG 65

QY 150 TGTGGCAGCTCCCTGAGTGCAGCTCTTAATCGCAGAGAGATCCAGGCCCTGGCCCC 209
 Db 66 TGTGGCAGCTCCCTGAGTGCAGCTCTTAATCGCAGAGAGATCCAGGCCCTGGCCCC 125

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 Db 126 CCAATCAGAAACCTATGACTCAACCGCTACTGAGAGATCACTCCGACCTTAGCTG 185

QY 270 GGACCTTACCTGAACCTACCTGGGGCCCCCTTTCAAGAGAGCTTCAATCTCTCTCGAC 329
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Db          752 CACT 755

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LOCUS      806 bp mRNA linear EST 02-DEC-2003
DEFINITION AGENCOURT_15196878 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:7002177 5', mRNA sequence.
CK130211
VERSION    1 (bases 1 to 806)
KEYWORDS   EST.
SOURCE     CK130211.1 GI:38622147
           Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 806)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgabbs-remail.nih.gov
           Tissue Procurement: Narayan Bhat
           cDNA Library Preparation: Bhat Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: IRBK4 row: e column: 07
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           /lab_host="DH5A (T1 phage-resistant)"
           /clone_lib="NIH_MGC_195"
           /note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:
           loxP-HindIII; Clones from this library have been
           PCR-amplified using gene-specific primers to contain the
           complete open reading frame (based on known gene sequences
           available from NCBI's RefSeq). Template for PCR is cDNA
           derived from either pooled cytoplasmic polyA RNA from 30
           cells lines or pooled total RNA from 10 different tissues
           (from BD Biosciences/Clontech and Washington University).
           PCR products are directionally cloned into the loxP sites
           of the pDNR-Dual vector. Library constructed by Dr.
           Narayan Bhat, Earl Bere III and Hongling Liao (Gene
           Expression Laboratory, Research Technology Program, SAIC
           Frederick, NCI-Frederick, Frederick, MD 21702). For
           information on which gene each clone represents, please
           visit our anonymous ftp site at
           ftp://image.llnl.gov/image/rearayed_plates/IRBK.presv.dat
           a Note: this is a NIH_MGC Library."
ORIGIN
Query Match      72.1%; Score 590.2; DB 14; Length 806;
Best Local Similarity 91.5%; Pred. No. 3.4e-121;
Matches 625; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
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DB 1 GGGACTCGTGGGGAGTGTAGCTTGCCTATGACGGTGTGTGGCAGCTTCCCTGCGAGTGC 60
QY 171 CAGCTCTTAATCGCACAGAGATCCAGGCGCTTCCATCCAGAGAGATCCAGAGAGATCCATGACC 230
DB 61 CAGCTCTTAATCGCACAGAGATCCAGGCGCTTCCATCCAGAGAGATCCATGACC 120
QY 231 TCACCGCTTACCTGAGGATCAACTCCGAGCTTACCTGAGCTTGGGACCTACCTGAGTACCTGG 290
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QY 351 GGGCCACGGTCAACTTGGAGTGTGGGAGCTCAATGACAGGCTGGGCTGAGGCTGAGCCAGA 410
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DB 361 CTGCTGAGCTGCGCGGACCTTCTGTGCTGAGCTTCTGTGCTGAGCTTCTGTGCTGAGCTTCT 420
QY 531 GCATTGAGCGGTACATGGCGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 590
DB 421 GCATTGAGCGGTACATGGCGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
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DB 481 AACCCACTTGGACTCTCTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCC 540
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DB 541 GGCTGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCT 600

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1 (bases 1 to 662)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 662)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Query Match          69.9%; Score 572.4; DB 29; Length 662;
Best Local Similarity 91.5%; Pred. No. 2.9e-117;
Matches 606; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 111 GGGACTCGTGGGGAGTGTAGCTTGCCTATGACGGTGTGTGGCAGCTTCCCTGCGAGTGC 170
DB 1 GGGACTCGTGGGGAGTGTAGCTTGCCTATGACGGTGTGTGGCAGCTTCCCTGCGAGTGC 60
QY 171 CAGCTCTTAATCGCACAGAGATCCAGGCGCTTCCATCCAGAGAGATCCAGAGAGATCCATGACC 230
DB 61 CAGCTCTTAATCGCACAGAGATCCAGGCGCTTCCATCCAGAGAGATCCATGACC 120
QY 231 TCACCGCTTACCTGAGGATCAACTCCGAGCTTACCTGAGCTTGGGACCTACCTGAGTACCTGG 290
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QY 351 GGGCCACGGTCAACTTGGAGTGTGGGAGCTCAATGACAGGCTGGGCTGAGGCTGAGCCAGA 410
DB 241 GGGCCACGTGTGACTTGGAGTGTGGGAGCTCAATGACAGGCTCAATGACAGGCTGAGCCAGA 300
QY 411 ACTATGAGCGGTACAGTCACTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
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QY 471 CAGCTGAATCCGAGCTGAGCTTGGCCCACTTCTGTACAGAGCTTCCAGGCTTCTGGGGA 530
DB 361 CTGCTGAGCTGCGCGGACCTTCTGTGCTGAGCTTCTGTGCTGAGCTTCTGTGCTGAGCTTCT 420
QY 531 GCATTGAGCGGTACATGGCGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 590
DB 421 GCATTGAGCGGTACATGGCGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 591 AGCCAGCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCT 650
DB 481 AACCCACTTGGACTCTCTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCC 540
QY 651 GGCTGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCT 710
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DEFINITION       Pan troglodytes HCM3468 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION        AY409171
VERSION          AY409171.1
KEYWORDS         GSS.
SOURCE           Pan troglodytes (chimpanzee)
ORGANISM         Pan troglodytes

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QY 711 AGAAGAAGATGAGGCTTCAGAGAGCTTCACTCAGCTTGGAGGACATGGTTCT 770
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QY 771 GA 772
Db 661 GA 662

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DEFINITION IMAGE:6197786 5', mRNA sequence.
ACCESSION BQ940483
VERSION BQ940483.1 GI:22355961
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1157)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13608 row: g column: 03
High quality sequence stop: 572.
Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="Lupski sciatic nerve"
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Directionally cloned using the following adaptors:
5'-TCGACCCAGCGTCCG-3' and
5'-GACTAGTCTTAGATCGGAGCGCGCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

ORIGIN
Query Match 69.4%; Score 568.6; DB 13; Length 1157;
Best Local Similarity 89.8%; Pred. No. 2.7e-116;
Matches 622; Conservative 0; Mismatches 69; Indels 2; Gaps 1;

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Db 58 AGGGAGCTCTGGGGATCTTAGCTTGCCTATGACGCTGTGTGGACCTCCCTGCAGT 117
QY 169 GCCAGCTCTTAATCGACAGGAGATCCAGGGCCCTGGCCCTCCATCCAGAAAACCTATGA 228
Db 118 GCCAGCTCTTAATCGACAGGAGATCCAGGGCCCTGGCCCTCCATCCAGAAAACCTATGA 177
QY 229 CCTACCCGCTACCTGGAGCATCACTCGGAGCTTAGCTGGACCTACCTGAACTACCT 288

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Db 178 CTTACCCGCTACTGAGGACCACTCCGAGCTTGGTGGGACCTATCTGAATACCT 237
QY 289 GGGGCCCCCTTTCAACGAGCCTGACTTCAATCTCTCGACTGGGGGCGAAGAACTCTGCC 348
Db 238 GGGGCCCCCTTTCAACGAGCCTGACTTCAACCTCTCCCGCTGGGGGCGAAGAACTCTGCC 297
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QY 529 CACATTTGAGGCTGTCAATGGCGACGCTTGGCTACCCACTGCCCCAGCCCTCTGCCAGGGAC 588
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QY 709 TAAGAAGAAGATGACGCTCCAGAGCTTCAGTCACTCCCTGCACTTGGAGG--CACATGGT 766
Db 658 CAAGAAGAAGATGACGCTCCAGAGCTTCAGTCACTCCCTGCACTTGGAGGCTCATGGGC 717
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Db 718 TTCTGACCTCTGACCTTAAACCCACACCTCC 750

RESULT 13
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DEFINITION mRNA sequence.
ACCESSION BQ164929
VERSION BQ164929.1 GI:12671563
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1053)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10244 row: m column: 14
High quality sequence start: 3
High quality sequence stop: 675.
Location/Qualifiers
1..1053
/organism="Homo sapiens"
/mol_type="mRNA"
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FEATURES
source

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Accession: BG437538.1 GI:13344044
Version: BG437538.1
Keywords: EST.
Source: Homo sapiens (human)
Organism: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 853)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: sgabbs-remail.nih.gov
Tissue Procurement: DCTD/DP/Genetics
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1384 row: i column: 19
High quality sequence stop: 761.
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/lab_host="DH10B (phage-resistant)"
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/note="Organ: lung; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

Query Match 66.4%; Score 544; DB 12; Length 1053;
Best Local Similarity 88.2%; Pred. No. 8.1e-111;
Matches 660; Conservative 0; Mismatches 80; Indels 8; Gaps 6;
QY 24 CGGGCTCGCCCTCCCACTCGCCAGCCTCTGGAGAGAGCGCGCCCGCGCGCGCG 83
Db 2 CGGGCTCGCCCTCCCACTCGCCAGCCTCTGGAGAGAGCGCGCGCGCGCGCG 61
QY 84 CCCCCAGCCCATGAGCCTCGAGAGAGGAGCTCTGGGGGATGTTAGCTTGCTATGCA 143
Db 62 CCCCCAGTCCCATGAGCCTCGAGAGAGGAGCTCTGGGGGATGTTAGCTTGCTATGCA 121
QY 144 CGGTGCTGGCAGCCTCCCTGCGAGTGCAGCTCTTAATGCGACAGAGATCCAGGCGCTG 203
Db 122 CGGTGCTGGCAGCCTCCCTGCGAGTGCAGCTCTTAATGCGACAGAGAGGAGCGCTG 181
QY 204 GCGGCTCCATCCAGAAACCTATGACCTACCCGCTACCTGAGAGCATCAACTCGGAGCT 263
Db 182 GCGGCTCCATCCAGAAACCTATGACCTACCCGCTACCTGAGAGCATCAACTCGGAGCT 241
QY 264 TAGTGGAGCCTACTGAACTACTTGGGGGCGCCG---TTTCAAGAGCCT-GACTTCAT 319
Db 242 TGGTGGAGCCTATCTGAACTAGCTTGGGGGCGCCGTTTCACTGAGCCTAGACTTCAAC 301
QY 320 CCTCTGAGCTGGGGGCGAGAACTCTG-CCAGGGCCACGCTCAACTTGAAGTGTGGCG 378
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QY 379 AAGCCTCAATGACAGGCTGGGCTGACCCAGAACTATGAGCGGTACAGTCACTCTCTGTG 438
Db 362 AAGCCTCAATGACAACTGGCGCTGACCCAGAACTAGAGGCGCTTACAGCCACTTCTGTG 421
QY 439 TTACTTGGTGGCTCAACCGTCAAGCTGCGACAGCTGAATCCGAGCTAGCTGGGCCCA 498
Db 422 TTACTTGGTGGCTCAACCGTCAAGCTGCGACAGCTGAATCCGAGCTAGCTGGGCCCA 481
QY 499 CTTCTGACAGCCTCCAGGGCTCTGCTGGGAGCATTTGCAAGTGTCAATGCGAGCTGG 558
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QY 559 CTACCCACTG-CCCCAGCCTCTGCGAGGACTG-AGCAGCCTGGGCGCCCTGGCCCTGCC 616
Db 542 CTACCCACTGCCCCAGCGCTGCTGGGAGCTGAACCCACTTTTGGACTCTCTGGCCCTTGC 601
QY 617 CACAGTGACTTCTCCAGAAATGATGACTTCTGGCTGTCTGAAGAGAGCTGCGAGCTGG 676
Db 602 CACAGTGACTTCTCCAGAAATGATGACTTCTGGCTGTCTGAAGAGAGCTGCGAGCTGG 661
QY 677 CATTGGGCTTCCAGCAAGGACTTCAACCGGCTTAAAGAGAGATGCGAGCTTCCAGAGCT 736
Db 662 CTGTGGCGCTCGGCC-AGGACTTCACCGGCTCCAGAGAGATGCGAGCTTCCAGAGCTT 720
QY 737 TCAGTCACTCTGAGCTTGGAGGACATG 764
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RESULT 14
BG437538
LOCUS 602489277p1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4621530 5',
DEFINITION mRNA sequence.

Accession: BG437538
Version: BG437538.1 GI:13344044
Keywords: EST.
Source: Homo sapiens (human)
Organism: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 853)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: sgabbs-remail.nih.gov
Tissue Procurement: DCTD/DP/Genetics
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1384 row: i column: 19
High quality sequence stop: 761.
Location/Qualifiers
1..853
/organism="Homo sapiens"
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/lab_host="DH10B (phage-resistant)"
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/note="Organ: lung; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

Query Match 66.3%; Score 543; DB 12; Length 853;
Best Local Similarity 88.8%; Pred. No. 1.2e-110;
Matches 667; Conservative 0; Mismatches 75; Indels 9; Gaps 7;
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QY 176 CTTAATCGCAGAGGATCCAGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 235
Db 120 CTTAATCGCAGAGGATCCAGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 179
QY 236 CGCTACTCTGAGCATCAACTCCGCGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 295
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QY 296 CTTTCAAGCGCTGACTTCAATCTCTCTGAGCTGGGGGAGAACTCTGCCAGGGCC 355
Db 240 CTTTCAAGCGCTGACTTCAATCTCTCTGAGCTGGGGGAGAACTCTGCCAGGGCC 299
QY 356 ACGGTCAACTTGAAGTGTGGGAGAGCGCTCAATGACAGGCTGCGGCTGACCCAGAACTAT 415
Db 300 ACTGTTGACTTGGAGGTGTGGGAGAGCGCTCAATGACAACTGCGGCTGACCCAGAACTAC 359
QY 416 GAGCGTACAGTCACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 475
Db 360 GAGCGCTACAGCACCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 419

ORIGIN

Result No.	Query			Length	DB	ID	Description
	Score	Match					
1	819	100.0	819	2	AAV22654	AAV22654	CDNA enco
2	819	100.0	819	2	AAV47512	AAV47512	Mouse neu
3	819	100.0	819	3	AAK39483	AAK39483	Murine NN
4	819	100.0	819	6	ABK11649	ABK11649	Mouse CDN
5	674	82.3	881	4	AAH74484	AAH74484	Nucleotid
6	674	82.3	1790	3	AAAB88546	AAAB88546	Human int
7	669.4	81.7	797	2	AAV22652	AAV22652	CDNA enco
8	669.4	81.7	797	2	AAV47510	AAV47510	Human neu
9	669.4	81.7	797	3	AAK39481	AAK39481	Human NNT
10	669.4	81.7	797	6	ABK11647	ABK11647	Human CDN
11	660	80.6	768	4	AAH99772	AAH99772	Human pro
12	646.4	78.9	648	3	AAAB88547	AAAB88547	Mouse int
13	627	76.6	1710	2	AAK16161	AAK16161	Human car
14	600.2	73.3	729	4	AAAD04201	AAAD04201	Human car
15	583.2	71.2	1008	4	AAK51548	AAK51548	Human pol
16	577	70.5	968	4	ABA09140	ABA09140	Human car
17	577	70.5	968	4	AAK52532	AAK52532	Human pol
18	429.6	52.5	5087	3	AAK39482	AAK39482	Human NNT
19	429.6	52.5	5087	6	ABK11648	ABK11648	Human nov
20	429.6	52.5	5088	2	AAV22653	AAV22653	Human gen
21	429.6	52.5	5088	2	AAV47511	AAV47511	Human neu
22	419.8	51.3	495	4	AAI25564	AAI25564	Probe #15
23	419.8	51.3	495	4	ABA17733	ABA17733	Human foe


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Db 1 TATTATTAAAGCTTGGCCGGAGCCGGCTGCGCTCCCTCCCACTCCGCCAGCCTCTGGGAGA 60
QY 61 GGAGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGG 120
Db 61 GGAGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGG 120
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Db 121 GGGGATGTAGCTTGGCTTATGACGGTGTGTGACCTCTCCCTCAGTGCAGCTCTTAA 180
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QY 241 CCGGAGCATCAACTCCGACCTTAGCTGGACCTACTGAACTACCTGGGGCCCCCTTT 300
Db 241 CCGGAGCATCAACTCCGACCTTAGCTGGACCTACTGAACTACCTGGGGCCCCCTTT 300
QY 301 CAACGAGCTGACTTCAATCTCTCTGACTGGGGGAGAACTCTGCCAGGGCCACGGT 360
Db 301 CAACGAGCTGACTTCAATCTCTCTGACTGGGGGAGAACTCTGCCAGGGCCACGGT 360
QY 361 CAACCTTGAAGTGGGGAAGCCTCAATGACAGGCTGCGGTGACCCAGAACTATGAGGC 420
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QY 421 GTACAGTCACTCTGTGTACTTGGTGGCTCAACCGTACAGCTGCCAGCTCCACAGTGAAT 480
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QY 601 GGGCCCTGGCCCTGCCACAGTACTTCTCCAGAACTGATGATCTTGGTGTCTGAA 660
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QY 661 GGAGCTGAGACCTGGCTATGGCTTCCAGCAAGGACTTCAACCGGCTTAAGAAGAGAT 720
Db 661 GGAGCTGAGACCTGGCTATGGCTTCCAGCAAGGACTTCAACCGGCTTAAGAAGAGAT 720
QY 721 GCAGCTCCAGCAGCTTCACTGACCTTCCAGTCTGAGGACATGGTTTCTGACCTCTGAC 780
Db 721 GCAGCTCCAGCAGCTTCACTGACCTTCCAGTCTGAGGACATGGTTTCTGACCTCTGAC 780
QY 781 CCTTAACCCCCACACCTCCAGGCCAGTCAAGCTGTGCTT 819
Db 781 CCTTAACCCCCACACCTCCAGGCCAGTCAAGCTGTGCTT 819

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RESULT 3

AAA39483

ID AAA39483 standard; cdna; 819 BP.

XX AC AAA39483;

XX AC AAA39483;

DT 24-AUG-2000 (first entry)

XX DE Murine NNT-1 cdna.

XX DE Murine NNT-1 cdna.

NNT-1; neurotrophic factor; neurotrophic; neuroprotective; treatment; anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological; nervous system degeneration; Alzheimer's disease; Parkinson's disease; Charcot-Marie-Tooth syndrome; Charcot-Marie-Tooth syndrome; murine; Huntington's disease; peripheral neuropathy; neural retina degeneration; retinopathy; immune disorder; hematopoietic disorder; ss.

Mus sp.

```

XX PH Key Location/Qualifiers
FT CDS 95..772
FT /*tag= a
FT /product= "NNT-1"
XX:
PN US6054294-A.
PD 25-APR-2000.
XX:
PF 12-DEC-1997; 97US-00988819.
XX:
PR 03-FEB-1997; 97US-00792019.
XX:
PA (AMGE-) AMGEN INC.
XX:
PI Chang M;
XX:
DR WPI; 2000-338492/29.
DR P-PSDB; AAY87814.
XX:
PT New nucleic acids encoding neurotrophic factors useful for stimulating
XX: growth of motor or sympathetic neurons for treating neuron cell damage.
XX:
PS Claim 2a; Fig 4; 42pp; English.
XX:
CC This invention describes a novel nucleic acid molecule (I) encoding a
CC novel neurotrophic factor (NNT-1) (II) which has neurotrophic,
CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic, and
CC ophthalmological activity. (I) is useful for producing NNT-1 polypeptides
CC which are useful for treating patients in whom various cells of the
CC central, autonomic, or peripheral nervous system have degenerated and/or
CC have been damaged by congenital disease, trauma, mechanical damage,
CC surgery, stroke, ischemia, infection, metabolic disease, nutritional
CC deficiency, malignancy and/or toxic agents. NNT-1 proteins are used to
CC treat diseases like Alzheimer's, Parkinson's, amyotrophic lateral
CC sclerosis, Charcot-Marie-Tooth syndrome, Huntington's disease, peripheral
CC neuropathy induced by diabetes or other metabolic disorders, and/or
CC dystrophies or degeneration of the neural retina such as retinitis
CC pigmentosa, drug-induced retinopathies, stationary forms of night
CC blindness, progressive cone-rod degeneration, immune disorders and
CC hematopoietic disorders. (II) is effective in treating neurological
CC conditions and promotes neuron regeneration. Neural functions are
CC effectively restored in patients suffering from various neurological
CC disorders. This sequence encodes the murine NNT-1 protein described in
CC the method of the invention
XX:
SQ Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 U; 0 Other;

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Query Match

Best Local Similarity 100.0%; Score 819; DB 3; Length 819;

Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TATTATTAAAGCTTCCCGGAGCCGGCTGCGCTCCCTCCCACTCCGCCAGCCTCTGGGAGA 60
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QY 61 GGAGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGG 120
Db 61 GGAGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGG 120
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Db 121 GGGGATGTAGCTTGGCTTATGACGGTGTGTGACCTCTCCCTCAGTGCAGCTCTTAA 180
QY 181 TCGCAGGAGATCCAGGCTTCCCTCCCTCCATCCAGAAACCTATGACCTCACCCTA 240
Db 181 TCGCAGGAGATCCAGGCTTCCCTCCCTCCATCCAGAAACCTATGACCTCACCCTA 240
QY 241 CCGGAGCATCAACTCCGACCTTAGCTGGACCTACTGAACTACCTGGGGCCCCCTTT 300
Db 241 CCGGAGCATCAACTCCGACCTTAGCTGGACCTACTGAACTACCTGGGGCCCCCTTT 300

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QY 301 CAACGAGCCTGACCTCAATCTCTCGACTGGGGGCAAACTCTGCCAGGGCCACGGT 360
Db 301 CAACGAGCCTGACCTCAATCTCTCGACTGGGGGCAAACTCTGCCAGGGCCACGGT 360
QY 361 CAACTTGAAGTGGGCAAGCCTCAATGACAGGCTGGGCTGACCCAGAACATGAGGC 420
Db 361 CAACTTGAAGTGGGCAAGCCTCAATGACAGGCTGGGCTGACCCAGAACATGAGGC 420
QY 421 GTACAGTCACTCTCTGTGTACTTGGTGGGCTCAACCGTCAAGCTGACAGCTGAAT 480
Db 421 GTACAGTCACTCTCTGTGTACTTGGTGGGCTCAACCGTCAAGCTGACAGCTGAAT 480
QY 481 CCGAGTGGGCGGCTGCTTCTGTACAGCTCCAGGCTGCTGGCAGCATGTCAGG 540
Db 481 CCGAGTGGGCGGCTGCTTCTGTACAGCTCCAGGCTGCTGGCAGCATGTCAGG 540
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Db 601 GGGCGCTGGGCGGCTGCTTCTGTACAGCTCCAGGCTGCTGGCAGCATGTCAGG 660
QY 661 GCGAGTGGGCGGCTGCTTCTGTACAGCTCCAGGCTGCTGGCAGCATGTCAGG 720
Db 661 GCGAGTGGGCGGCTGCTTCTGTACAGCTCCAGGCTGCTGGCAGCATGTCAGG 720
QY 721 GCAGCTCCAGGCTGCTTCTGTACAGCTCCAGGCTGCTGGCAGCATGTCAGG 780
Db 721 GCAGCTCCAGGCTGCTTCTGTACAGCTCCAGGCTGCTGGCAGCATGTCAGG 780
QY 781 CCTTAACCCCACTCCAGGCTGCTTCTGTACAGCTCCAGGCTGCTGGCAGCAT 819
Db 781 CCTTAACCCCACTCCAGGCTGCTTCTGTACAGCTCCAGGCTGCTGGCAGCAT 819

RESULT 4
ABK11649
ID ABK11649 standard; cDNA; 819 BP.
XX AC ABK11649;
XX XX
DT 05-JUN-2002 (first entry)
XX DE Mouse cDNA encoding novel neurotrophic factor NNT1.
XX Mouse; ss; gene; NNT1; neurotrophic factor; IgE-related disease;
KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
KW vascular restenosis; rheumatoid arthritis; psoriatic joint disease;
KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
KW inflammatory bowel disease; transplant rejection; reproductive disorder;
KW graft versus host disease; infertility; miscarriage; preterm labour.
XX OS Mus sp.
XX XX
XX PH Location/Qualifiers
XX CDS 95..772
XX FT /*tag= a
XX FT /product= "NNT1"
XX XX
XX PN WO200215977-A2.
XX XX 28-FEB-2002.
XX XX 17-AUG-2001; 2001WO-US025906.
XX XX 18-AUG-2000; 2000US-0226436P.
XX XX 16-AUG-2001; 2001US-00931704.
XX XX (AMGE-) AMGEN INC.
XX PA

XX Senaldi G;
PI WPI; 2002-280867/32.
XX P-PSDB; AAU78177.
DR Treating Immunoglobulin E-related disease, modulating IgE levels in a
XX patient, preventing IgE-related disease and treating allergic diseases,
PT involves administering NNT-1 inhibitor to a patient.
PT
XX
XX Claim 2; Fig 4; 63pp; English.
XX The invention relates to treating Immunoglobulin E (IgE)-related disease,
CC modulating IgE levels in a patient, preventing an IgE-related disease,
CC and treating allergic diseases, comprising administering a
CC therapeutically effective amount of novel neurotrophic factor (NNT)-1
CC inhibitor to a patient. Also included are a method of diagnosing an IgE-
CC related disease or susceptibility to an IgE-related disease, by
CC determining the presence or amount of expression of an NNT1 polypeptide
CC encoded by a NNT1 nucleotide sequence, its fragment or naturally
CC occurring variant, and diagnosing an IgE-related disease or
CC susceptibility of an IgE-related disease based on the presence or amount
CC of expression of the polypeptide and a pharmaceutical composition for use
CC in treating IgE-related disease, comprising the NNT1 inhibitor. The NNT1
CC inhibitor is useful for preventing and treating IgE-related disease,
CC modulating IgE levels, and treating allergic diseases e.g. Type I
CC allergic disease, allergic rhinitis, eczema, dermatitis, pollinosis,
CC asthma, immune diseases and disorders, diseases involving abnormal cell
CC proliferation including cancer, arteriosclerosis and vascular restenosis,
CC diseases and conditions relating to dysfunction of immune system
CC including rheumatoid arthritis, psoriatic joint disease, autoimmune
CC arthritis, osteoarthritis, inflammatory joint disease, inflammatory
CC disease, multiple sclerosis, lupus, diabetes, inflammatory bowel disease,
CC transplant rejection, and graft versus host disease, and reproductive
CC diseases and disorders including infertility, miscarriage, preterm labour
CC and delivery, and endometriosis. The present sequence encodes mouse NNT1
XX
XX Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 U; 0 Other;

Query Match 100.0%; Score 819; DB 6; Length 819;
Best Local Similarity 100.0%; Pred. No. 2.8e-194;
Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATATTAAAGCTTCGCGGAGCGCGGCTCGCCCTCCACCTCCGAGCCTCGGAGTCTGGAGA 60
Db 1 TATATTAAAGCTTCGCGGAGCGCGGCTCGCCCTCCACCTCCGAGCCTCGGAGTCTGGAGA 60
QY 61 GGAGCG 120
Db 61 GGAGCG 120
QY 121 GGGGATTTAGCTTGGCTATGACAGGCTGTGTGGCACTCCCTCGAGTGCACCTCTTAA 180
Db 121 GGGGATTTAGCTTGGCTATGACAGGCTGTGTGGCACTCCCTCGAGTGCACCTCTTAA 180
QY 181 TCGCACAGGAGATCCAGGCGCTCGCCCTCCATCCAGAAACCTATGACCTACCCGCTA 240
Db 181 TCGCACAGGAGATCCAGGCGCTCGCCCTCCATCCAGAAACCTATGACCTACCCGCTA 240
QY 241 CCTGGAGATCAACTCCGAGCTTAGTGGAGCTTACCTGAATCTCTGGGGCCCTTTT 300
Db 241 CCTGGAGATCAACTCCGAGCTTAGTGGAGCTTACCTGAATCTCTGGGGCCCTTTT 300
QY 301 CAACGAGCTGACTTCAATCTCTCGACTGGGGGAGAAACTCTGCCAGGGCCACGGT 360
Db 301 CAACGAGCTGACTTCAATCTCTCGACTGGGGGAGAAACTCTGCCAGGGCCACGGT 360
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Db 361 CAACTTGAAGTGGGCAAGCCTCAATGACAGGCTGGGCTGACCCAGAACATGAGGC 420
QY 421 GTACAGTCACTCTCTGTGTACTTGGTGGGCTCAACCGTCAAGCTGACAGCTGAAT 480

662	QY	GAGCTGACAGCCTGGCTATGGCGTTTCAGCCAGGACTTCAACCGGCTTAAGAAGAAGATG	721
741	Db	GAGCTGCAGACCTGGCTGTGGCGCTCGGCCAAGGACTTCAACCGGCTCAAGAAGAAGATG	800
722	QY	CAGCCTCCAGAGCTTCAGTCAACCTCGACTTGGAGGCACATGGTTTCTGACCTCTGACC	781
801	Db	CAGCCTCCAGCAGTGCAGTCAACCTGACCTGGGGGCTCATGGCTTCGACTTCTGACC	860
782	QY	CT	783
861	Db	TT	862

RESULT 6	
AAA88546	
ID	AAA88546 standard; DNA; 1790 BP.
XX	
XX	
AC	AAA88546;
XX	
DT	22-JAN-2001 (first entry)
XX	
DE	Human interleukin-B60 (IL-B60) gene.
XX	
XX	Interleukin-B60; IL-B60; human; cytokine; chromosome 11;
KW	cytokine-like factor-1; haematopoietic; inflammation; antiinflammatory;
KW	autoimmune disease; therapy; ds.

CC	inflammatory or autoimmune disorders and also for drug screening. The
CC	IL60B gene maps to human chromosome 11
XX	
SSQ	Sequence 1790 BP; 381 A; 560 C; 474 G; 375 T; 0 U; 0 Other;
	Query Match 82.3%; Score 674; DB 3; Length 1790;
	Best Local Similarity 92.2%; Pred. No. 4.7e-158;
	Matches 721; Conservative 0; Mismatches 60; Indels 1; Gaps 1;
QY	2 ATTATTAAAGCTTCGCGAGCGGGGTGCGCTCCCACTCCGCCAGCCTCTGGAGAG 61
DB	40 ATTATTAAAGCTTCGCGAGCGGGGTGCGCTCCCACTCCGCCAGCCTCTGGAGAG 99
QY	62 GAGCG 121
DB	100 GAGCG 158
QY	122 GGGATGTTAGCTTTCATGTGACGGTGCTGTGGCACTCCCTCGAGTGCCAGACTCTTAAT 181
DB	159 GGGATGTTAGCTTTCATGTGACGGTGCTGTGGCACTCCCTCGAGTGCCAGCTCAAT 218
QY	182 CGCACAGGAGATCCAGCGCGCTGCGCGCTCCATCCAGAAAACCTATGACCTCAACCGCTAC 241
DB	219 CGCACAGGAGATCCAGCGCGCTGCGCGCTCCATCCAGAAAACCTATGACCTCAACCGCTAC 278
QY	242 CTGAGAGCATCAACTCCGCGAGCTTAGCTGGAGCCTTACCTGAACTACCTGGGGCGCCCTTC 301
DB	279 CTGAGAGCATCAACTCCGCGAGCTTAGCTGGAGCCTTACCTGAACTACCTGGGGCGCCCTTC 338
QY	302 AACGAGCGCTGACTTCAATCTCTCTGACTGGGGGAGAAAACCTGCCAGGGCCACGGCTC 361
DB	339 AACGAGCGAGACTTCAACCTCTCCCGCTGGGGGAGAGACTCTGCCAGGGCCACCTGTT 398
QY	362 AACTTGGAACTGTGGCGAAGCCTCAATGACAGGCTGCGGCTGACCCAGAACTATGAGCGG 421
DB	399 GACTTGGAGGTGTGGCGAAGCCTCAATGACAAACCTGCGGCTGACCCAGAACTACGAGGCC 458
QY	422 TACAGTCACCTCTCTGTGTTACTTTCGCTGGCTCAACCGCTCAGGGTGCCACAGCTGAATC 481
DB	459 TACAGCCACCTTCTGTGTTACTTTCGCTGGCTCAACCGCTCAGGGTGCCACCTGCTGAGCTG 518
QY	482 CGAGCTAGCTGCGCCCACTTCTGTACAGCCTCCAGGGCTGCTGGGGAGCATTTGCAAGT 541
DB	519 CGCGCAGCCTGCGCCCACTTCTGCACAGCCTCCAGGGCTGCTGGGGAGCATTTGCGGGC 578
QY	542 GTCATGGGAGCGCTGGCTACCCACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 601
DB	579 GTCATGGGAGCGCTGGGCTACCCACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 638
QY	602 GCCCGTGGCGCTGCCCACTGACTTCTCCAGAAAGATGGATGACTTCTGCTGCTGAAG 661
DB	639 ACTCTGGCGCTGCCCACTGACTTCTCTCCAGAAAGATGGACGACTTCTGGCTGCTGAAG 698
QY	662 GAGCTGACAGCCTGGCTATGGCGTTTACGCCAGGACTTCAACCGGCTTAAGAAAGATG 721
DB	699 GAGCTGACAGCCTGGCTATGGCGTTTACGCCAGGACTTCAACCGGCTTCAAGAAAGATG 758
QY	722 CAGCGCTCCAGCAGCTTCAGTTCACCTGCACTTTGGAGGCACATGGTTTCTGACCTTCAACC 781
DB	759 CAGCGCTCCAGCAGCTTCAGTTCACCTGCACTTTGGAGGCCTCAAGGCTTCTGACTTCTGACC 818
QY	782 CT 783
DB	819 TT 820

RESULT 7
AAV22652
ID AAV22652 standard; cDNA; 797 BP.
XX
XX AAV22652;
XX
DT 13-JUL-1998 (first entry)

XX cDNA encoding human neurotrophic factor NNT-1.
 XX Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
 KW treatment; neurological disease; degeneration; Parkinson's disease;
 KW amyotrophic lateral sclerosis; ALS; Alzheimers's disease; stroke; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH CDS 90..767
 FT /*tag= a
 FT sig_peptide 90..170
 FT /*tag= b
 FT mat_peptide 171..764
 FT /*tag= c
 XX US5741772-A.
 PN XX
 XX 21-APR-1998.
 PD XX
 XX 03-FEB-1997; 97US-00792019.
 PF XX
 XX 03-FEB-1997; 97US-00792019.
 PR XX
 XX (AMGE-) AMGEN INC.
 PA XX
 XX Chang M;
 PI XX
 XX WPI; 1998-260526/23.
 DR P-PSDB; AAW56141.
 XX Neurotrophic factor NNT-1 polypeptide and related nucleic acids - useful
 PT for stimulating growth of motor and sympathetic neurons.
 PT
 XX Disclosure; Fig 1; 41pp; English.
 XX
 CC The present sequence encodes a human neurotrophic factor, designated NNT-
 CC 1, which is capable of stimulating growth of motor or sympathetic
 CC neurons. The NNT-1 protein is useful in the treatment of neurological
 CC diseases characterised by the degeneration and death of particular
 CC classes of neurons. These diseases specifically include Parkinson's
 CC disease, amyotrophic lateral sclerosis (ALS), Alzheimers's disease, stroke
 CC and various degenerative disorders affecting vision
 XX
 SQ Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 U; 0 Other;
 Query Match 81.7%; Score 669.4; DB 2; Length 797;
 Best Local Similarity 92.0%; Pred. No. 5.5e-157;
 Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
 5 ATTAAGCTTCGGCGAGCGCGGCTCGCCCTCCACTCCGCGAGCTCTGGGAGAGGAG 64
 1 ATTAAGCTTCGGCGAGCGCGGCTCGCCCTCCACTCCGCGAGCTCTGGGAGAGGAG 60
 65 CCGCGCCG 124
 61 CCGCACC CG 119
 125 ATGTTAGCTTTCGCTATGACAGGCTGCTGGACCTCCCTCGAGTCCAGCTTTAATCGC 184
 120 ATGTTAGCGTGCTGTCAGCGTGCTGCGACCTCCCTCGAGTCCAGCTCTCAATCGC 179
 185 ACAGGAGATCCAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 244
 180 ACAGGGACCGAGCG 239
 245 GAGCATCAACTCCGACCTTAGCTGGGACCTACTGAACTACCTGGGCGCGCGCG 304
 240 GAGCACCACCTCCGACCTTGGCTGGACCTATCTGAACTACCTGGGCGCGCGCG 299
 305 GAGCTGACTTCAATCTCTCGAGCTGGGGCGGAGAACTCTGCCAGGCGCAGCGTCAAC 364

300 GAGCCAGACTTCAACCCCTCCCGCTCGGGGCGAGAGACTCTGCCAGGGCCACTGTTGAC 359
 365 TTGGAAGTGTGGCGAGGCTCAATGACAGGCTGCGGTGAGCCAGAACTATGAGCGGTAC 424
 360 TTGGAGGTGTGGCGAGGCTCAATGACAACTGCGGTGAGCCAGAACTATGAGCGGTAC 419
 425 AGTCACCTCCCTGTGTACTTGGCTGAGCTCAACCGTCAAGGCTGCCACAGCTGAACTCCGA 484
 420 AGCCACCTTCTGTGTACTTGGCTGAGCTCAACCGTCAAGGCTGCCACTGCTGAGCTGGC 479
 485 CGTAGCTTGGCGCGCTTCTGTACAGGCTCCAGGCGCTGCTGGGCGAGCAATTGCGAGTGC 544
 480 CGCAGCTTGGCGCGCTTCTGTACAGGCTCCAGGCGCTGCTGGGCGAGCAATTGCGGCGCTC 539
 545 ATGCGAGCGCTTGGCTACCCACTGCCAGCTCTGCCAGGAGCTGAGCCAGCTTGGGCC 604
 540 ATGCGAGCTTGGCTACCCACTGCCAGCTCTGCCAGGCGCTGCTGGGAGTGAACCCACTTGG 599
 605 CTTGCGCTTGGCGCGCTTCTGTACAGGCTTCTCCAGAGGATGATGACTTCTGGCTCTGAAG 664
 600 CTTGCGCTTGGCGCGCTTCTGTCCAGAGGATGAGAGCTTCTGGCTCTGTAAGGAG 659
 665 CTGAGAGCTTGGCTATGGCTTCCAGGAGCTTCAACCGCTTAAAGAGAGATGAG 724
 660 CTGAGAGCTTGGCTATGGCTTCCAGGAGCTTCAACCGCTTAAAGAGAGATGAG 719
 725 CTTGAGAGCTTCACTCAGCTCAGCTTGGAGGCGACATGCTTCTGACCTCTGACCT 783
 720 CTTGAGAGCTTCACTCAGCTCAGCTTGGAGGCGCTCATGCTTCTGACTTCTGACCTT 778
 RESULT 8
 AAV47510
 ID AAV47510 standard; cDNA; 797 BP.
 XX
 AC AAV47510;
 XX
 DT 09-NOV-1998 (first entry)
 DE Human neurotrophic factor NNT-1 cDNA.
 XX
 KW NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
 KW peripheral neuropathy; dystrophy; neural retina degeneration;
 KW common variable immunodeficiency; CVID; selective IGA deficiency;
 KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
 KW therapy; ss.
 KW Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 90..767
 FT /*tag= a
 FT sig_peptide 90..170
 FT /*tag= b
 FT mat_peptide 171..764
 FT /*tag= c
 XX
 PN WO9833922-A1.
 XX
 PD 06-AUG-1998.
 XX
 XX 02-FEB-1998; 98WO-US002363.
 PF XX
 XX 03-FEB-1997; 97US-00792019.
 PR 30-JAN-1998; 98US-00016534.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Chang M, Elliot GS, Senaldi G, Sarmiento U;
 XX WPI; 1998-437475/37.
 DR

DR P-PSDB; AAW29715.
 XX Newly isolated nucleic acid encoding human or murine neurotrophic factor
 PT NNT-1 - useful for treatment of neurological and immunological diseases
 PT or inflammation, also as vaccine adjuvant.
 XX
 XX
 PS Claim 3; Fig 1; 120pp; English.
 XX
 CC This newly isolated human cDNA sequence (deposited at ATCC 98295) codes
 CC for a novel neurotrophic factor, designated NNT-1 (see AAW29715), that is
 CC a growth factor for neurons and for B or T cells. It was obtained from a
 CC T-cell lymphoma cDNA library by expressed sequence tag analysis on the
 CC basis of homology to CNTF. The isolated NNT-1 cDNA was used as probe to
 CC isolated NNT-1 genomic DNA (see AAW29715). Vectors containing the cDNA or
 CC genomic DNA and host cells are provided for use in the production of NNT-
 CC 1 polypeptides. These are used to treat: (i) neurological or
 CC immunological diseases, specifically Alzheimer's, Parkinson's or
 CC Huntington's diseases, amyotrophic lateral sclerosis, Charcot-Marie-Tooth
 CC syndrome, peripheral neuropathy, dystrophy and degeneration of the neural
 CC retina, or conditions characterised by T or B cell defects, e.g. common
 CC variable immunodeficiency (CVID), selective IgA deficiency,
 CC hypogammaglobulinemia and X-linked agammaglobulinemia (claimed), but
 CC many others disclosed; and (ii) inflammation. NNT-1 is also able to boost
 CC immunoreactivity and antibody production following vaccination, and,
 CC since it inhibits tumour necrosis factor production, it may also be
 CC useful for treating sepsis. NNT-1 nucleic acid fragments are also used as
 CC hybridisation probes in diagnostic assays. In addition, cells that have
 CC been engineered to express NNT-1 can be implanted, or nucleic acids are
 CC delivered in gene therapy vectors
 XX
 SQ Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 U; 0 Other;
 Query Match 81.7%; Score 669.4; DB 2; Length 797;
 Best Local Similarity 92.0%; Pred. No. 5.5e-157;
 Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
 5 ATAAAGCTTCGCGAGCGCGGCTCGCCCTCCACCTCCGCGAGCTTCGGGAGAGAG 64
 1 ATAAAGCTTCGCGAGCGCGGCTCGCCCTCCACCTCCGCGAGCTTCGGGAGAGAG 60
 65 CG 124
 61 CCGCACCG 119
 125 ATGTTAGCTTGCTATGCAAGCTGTGTGGCACTTCCTGAGTCCAGCTTTAATCGC 184
 120 ATGTTAGCTTGCTATGCAAGCTGTGTGGCACTTCCTGAGTCCAGCTTTAATCGC 179
 185 ACAGGAGATCCAGGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 244
 180 ACAGGAGATCCAGGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 239
 245 GAGCATCAACTCCGAGCTTAGCTGGGACCTACCTGAACTACCTGGGCGCGCGCG 304
 240 GAGCATCAACTCCGAGCTTAGCTGGGACCTATCTGAACTACCTGGGCGCGCGCG 299
 305 GAGCATCAACTCAATCTCTGAGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 364
 300 GAGCATCAACTCAATCTCTGAGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 359
 365 TTGGAAGTGTGCGGAGCGCTCAATACAGGCTTGGCGCTGACCCGAGCAATGAGGCGCTAC 424
 360 TTGGAAGTGTGCGGAGCGCTCAATACAGCAACTGGCGCTGACCCGAGCAATGAGGCGCTAC 419
 425 ATCACTCTCTGTTACTTGGCGGCTCAACCGTCAAGCTGAGGCTGCAAGCTGAATCGGA 484
 420 AGCCACCTTCTGTGTACTTGGCGGCTCAACCGTCAAGCTGAGGCTGCAAGCTGAGCTGCGC 479
 485 CTTAGCTGGCGCGCTTCTGTACCAAGCTTCCAGGCGCTGCTGGGCGAGCAATGAGGCTGTC 544
 480 CGACGCTGGCGCGCTTCTGTACCAAGCTTCCAGGCGCTGCTGGGCGAGCAATGAGGCTGTC 539
 545 ATGCGGAGCGCTTGGGCTACCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 604

Db 540 ATGGGAGCTCTGGGTACCACTGCCAGCGCTTCCGCTGGGAGTGAACCACTTGGACT 599
 Qy 605 CTTGGCCCTGCCACAGTACTTCTCCAGAGATGGATGACTTCTGGCTGTGAAGGAG 664
 Db 600 CTTGGCCCTGCCACAGTACTTCTCCAGAGATGGATGACTTCTGGCTGTGAAGGAG 659
 Qy 665 CTGCAAGCTGTGCTTGGGTTTCCAGGAGTCTTCAACCGCTTAAAGAGATGCGAG 724
 Db 660 CTGCAAGCTGTGCTTGGGTTTCCAGGAGTCTTCAACCGCTTAAAGAGATGCGAG 719
 Qy 725 CTTCCAGCAGCTTCACTACCTCCGCTTGGAGGACATGTTTCTGACCTTGAACCT 783
 Db 720 CTTCCAGCAGCTTCACTACCTCCGCTTGGAGGACATGTTTCTGACCTTGAACCT 778
 RESULT 9
 AAA39481
 ID AAA39481 standard; cDNA; 797 BP.
 AC AAA39481;
 XX 24-AUG-2000 (first entry)
 DT Human NNT-1 cDNA.
 DE
 XX
 XX NNT-1; human; neurotrophic factor; nontropic; neuroprotective; treatment;
 KW anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
 KW nervous system degeneration; Alzheimer's disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
 KW Huntington's disease; peripheral neuropathy; neural retina degeneration;
 KW retinopathy; immune disorder; hematopoietic disorder; ss.
 XX Homo sapiens.
 OS
 XX
 XX
 PH Key Location/Qualifiers
 FT CDS 90..767
 FT /*tag= a
 FT /product= "NNT-1"
 XX
 PN US6054294-A.
 XX
 XX 25-APR-2000.
 PD
 XX
 XX 12-DEC-1997; 97US-00988819.
 PF
 XX 03-FEB-1997; 97US-00792019.
 PR
 XX (AMGB-) AMGEN INC.
 PA
 XX Chang M;
 PI
 XX WPI; 2000-338492/29.
 DR P-PSDB; AAY87813.
 XX
 XX New nucleic acids encoding neurotrophic factors useful for stimulating
 PT growth of motor or sympathetic neurons for treating neuron cell damage.
 PT
 XX Claim 1a; Fig 1; 42pp; English.
 PS
 XX This invention describes a novel nucleic acid molecule (I) encoding a
 CC novel neurotrophic factor (NNT-1) (II) which has nontropic,
 CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
 CC ophthalmological activity. (I) is useful for producing NNT-1 polypeptides
 CC which are useful for treating patients in whom various cells of the
 CC central, autonomic, or peripheral nervous system have degenerated and/or
 CC have been damaged by congenital disease, trauma, mechanical damage,
 CC surgery, stroke, ischemia, infection, metabolic disease, nutritional
 CC deficiency, malignancy and/or toxic agents. NNT-1 proteins are used to
 CC treat diseases like Alzheimer's, Parkinson's, amyotrophic lateral
 CC sclerosis, Charcot-Marie-Tooth syndrome, Huntington's disease, peripheral
 CC neuropathy induced by diabetes or other metabolic disorders, and/or
 CC dystrophies or degeneration of the neural retina such as retinitis

CC pigmentosa, drug-induced retinopathies, stationary forms of night
 CC blindness, progressive cone-rod degeneration, immune disorders and
 CC hematopoietic disorders. (I) is effective in treating neurological
 CC conditions and promotes neuron regeneration. Neural functions are
 CC effectively restored in patients suffering from various neurological
 CC disorders. This sequence encodes the human NNT-1 protein described in the
 CC method of the invention

XX SQ Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 U; 0 Other;

Query Match 81.7%; Score 669.4; DB 3; Length 797;
 Best Local Similarity 92.0%; Pred. No. 5.5e-157;
 Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 5 ATTAAGCTTCGCGGAGCGCGGCTCGCTCCCTCCACTCCGCGAGCGCTCTGGGAGAGGAG 64
 Db |||||
 1 ATTAAGCTTCGCGGAGCGCGGCTCGCTCCCTCCACTCCGCGAGCGCTCTGGGAGAGGAG 60
 QY 65 CCGCGCCCG 124
 Db |||||
 61 CCGCACCG 119
 QY 125 ATGTTAGCTTGCCTATGACAGGNGCTGTGGACCTCCCTCCAGTGCAGCTCTTAATCGC 184
 Db |||||
 120 ATGTTAGCTTGCCTATGACAGGNGCTGTGGACCTCCCTCCAGTGCAGCTCTTAATCGC 179
 QY 185 ACAGGAGATCCAGCGCTGCG 244
 Db |||||
 180 ACAGGAGATCCAGCGCTGCG 239
 QY 245 GAGCATCAACTCCGAGCTTAGCTGGGACCTTACCTGAACCTACCTGGGGCGCGCGCGCG 304
 Db |||||
 240 GAGCACCAACTCCGAGCTTAGCTGGGACCTTACCTGAACCTACCTGGGGCGCGCGCGCG 299
 QY 305 GAGCTGACTTCAATCTCTCTGACTGGGGCGAGAACTCTGCCAGGGCGCACGTCAC 364
 Db |||||
 300 GAGCGAGACTTCAACCTCTCCCGCTGGGGCGAGAGACTCTGCCAGGGCGCACGTCGAC 359
 QY 365 TTGGAAGTGTGGCGAAGCCTCAATGACAGGCTGGCGCTGACCCAGAACCTATGAGGGGTAC 424
 Db |||||
 360 TTGGAAGTGTGGCGAAGCCTCAATGACAGGCTGGCGCTGACCCAGAACCTATGAGGGGTAC 419
 QY 425 AGTCACCTCTCTGTTACTTGGTGGCGCTCAACCGTCAGCTGCCAGCTGCAACTCCGA 484
 Db |||||
 420 AGCCACCTTCTGTGTTACTTGGTGGCGCTCAACCGTCAGCTGCCAGCTGCAACTGCGC 479
 QY 485 CGTAGCTGGCCACTTCTGTACAGCTCCAGGGCTGTGGCGAGCACTTGCAGTGTC 544
 Db |||||
 480 CGTAGCTGGCCACTTCTGTACAGCTCCAGGGCTGTGGCGAGCACTTGCAGTGTC 539
 QY 545 ATGCGGACGCTTGGCTACCCACTGCGCGCGCTGTGCCAGGGACTGAGCGAGCTGGGCC 604
 Db |||||
 540 ATGCGGACGCTTGGCTACCCACTGCGCGCGCTGTGCCAGGGACTGAGCGAGCTGGACT 599
 QY 605 CTGCGCGCTGCGGACGAGTCTCTCCAGAGATGATGACTTGGCTGTGAGGAG 664
 Db |||||
 600 CTGCGCGCTGCGGACGAGTCTCTCCAGAGATGATGACTTGGCTGTGAGGAG 659
 QY 665 CTGCGAGCTGGCTATGCGGTTAGCGCAAGGACTTCAACCGGCTTAAGAGAGAGATGCGAG 724
 Db |||||
 660 CTGCGAGCTGGCTATGCGGTTAGCGCAAGGACTTCAACCGGCTTAAGAGAGAGATGCGAG 719
 QY 725 CCTCCAGAGCTTCAGTCAACCTGCTCACTTGGAGGACATGGTTCTGACCTCTGACCCCT 783
 Db |||||
 720 CCTCCAGAGCTTCAGTCAACCTGCTCACTTGGAGGACATGGTTCTGACCTCTGACCCCT 778

RESULT 10

ABK11647

ID ABK11647 standard; cDNA; 797 BP.

XX

AC ABK11647;

XX

DT 05-JUN-2002 (first entry)
 XX Human cDNA encoding novel neurotrophic factor NNT1.
 KW Human; ss; gene; NNT1; neurotrophic factor; IGE-related disease;
 KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
 KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
 KW vascular restenosis; rheumatoid arthritis; psoriatic arthritis;
 KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
 KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
 KW inflammatory bowel disease; transplant rejection; reproductive disorder;
 KW graft versus host disease; infertility; miscarriage; preterm labour.
 XX Homo sapiens.

OS XX
 FH Key Location/Qualifiers
 FT CDS 90..767
 FT /*tag= a
 FT /product= "NNT1"

XX WO200215977-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US025906.

XX 18-AUG-2000; 2000US-0226436P.

XX 16-AUG-2001; 2001US-00931704.

XX (AMGE-) AMGEN INC.

XX Senaldi G;

XX WPI; 2002-280867/32.

XX P-PSDB; AAU78176.

XX Treating Immunoglobulin E-related disease, modulating IGE levels in a
 PT patient, preventing IGE-related disease and treating allergic diseases,
 PT involves administering NNT-1 inhibitor to a patient.

XX Claim 2; Fig 1; 63pp; English.

XX The invention relates to treating Immunoglobulin E (IGE)-related disease,
 CC modulating IGE levels in a patient, preventing an IGE-related disease,
 CC and treating allergic diseases, comprising administering a
 CC therapeutically effective amount of novel neurotrophic factor (NNT)-1
 CC inhibitor to a patient. Also included are a method of diagnosing an IGE-
 CC related disease or susceptibility to an IGE-related disease, by
 CC determining the presence or amount of expression of an NNT1 polypeptide
 CC encoded by a NNT1 nucleotide sequence, its fragment or naturally
 CC occurring variant, and diagnosing an IGE-related disease or
 CC susceptibility of an IGE-related disease based on the presence or amount
 CC of expression of the polypeptide and a pharmaceutical composition for use
 CC in treating IGE-related disease, comprising the NNT1 inhibitor. The NNT1
 CC inhibitor is useful for preventing and treating IGE-related disease,
 CC modulating IGE levels, and treating allergic diseases e.g. Type I
 CC allergic disease, allergic rhinitis, eczema, dermatitis, pollinosis,
 CC asthma, immune diseases and disorders, diseases involving abnormal cell
 CC proliferation including cancer, arteriosclerosis and vascular restenosis,
 CC diseases and conditions relating to dysfunction of immune system
 CC including rheumatoid arthritis, psoriatic arthritis, inflammatory
 CC arthritis, osteoarthritis, inflammatory joint disease, autoimmune
 CC disease, multiple sclerosis, lupus, diabetes, inflammatory bowel disease,
 CC transplant rejection, and graft versus host disease, and reproductive
 CC diseases and disorders including infertility, miscarriage, preterm labour
 CC and delivery, and endometriosis. The present sequence encodes human NNT1

XX SQ Sequence 797 BP; 139 A; 297 C; 218 G; 143 T; 0 U; 0 Other;

Query Match

Best Local Similarity 81.7%; Score 669.4; DB 6; Length 797;

Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;


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QY 242 CTGAGGATCACTCCGAGCTTATAGCTGGGACCTTACCTGAACCTACCTGGGGCCCCCTTTC 301
Db 241 CTGGAGCACCACCTCCGAGCTTGGCTGGGACCTATCTGAACCTACCTGGGGCCCCCTTTC 300
QY 302 AACGAGCTGACTTCAATCCCTCCCTCGACTGGGGCGAAGAACTCTGCCAGGGCCACGGTC 361
Db 301 AACGAGCAGACTTCAACCTCCCGCTGGGGCGAGAGACTCTGCCAGGGCCACCTGTT 360
QY 362 AACTTGAAGTGTGGGAGGCTCAATGACAGGCTCGGGGTGACCCAGAACTATGAGGG 421
Db 361 GACTTGGAGTGTGGGAGGCTCAATGACAAACTCGGGGTGACCCAGAACTACGAGGC 420
QY 422 TACAGTCACTCCCTGCTTACTCGCTGGCTCAACCTCAGGCTGAGCTGACTGACTC 481
Db 421 TACAGCACCCTTCTGTACTCGCTGGCTCAACCTCAGGCTGAGCTGCTGACTG 480
QY 482 CGACGTAGCTGGGCCACTTCTGTACCAGGCTCCAGGGCCCTGCTGGGACGATTCAGGT 541
Db 481 CGCGGAGCTGGGCCACTTCTGTACCAGGCTCCAGGGCCCTGCTGGGACGATTCAGGT 540
QY 542 GTATGGGAGCTTGGCTTACCACTGCTCCAGGCTCTGCCAGGACTGAGCCAGCTGG 601
Db 541 GTATGGGAGCTTGGCTTACCACTGCTCCAGGCTCTGCCAGGACTGAGCCAGCTGG 600
QY 602 GCCCTGGCCCTGCCCACAGTGACTTCTCCAGAGATGATGACTTCTGCTGCTGAAG 661
Db 601 ACTCTGGCCCTGCCCACAGTGACTTCTCCAGAGATGATGACTTCTGCTGCTGAAG 660
QY 662 GAGTGCAGACTGGCTATGGCGTTAGCCAGGACTTCAACCGGCTTAAAGAGATG 721
Db 661 GAGTGCAGACTGGCTATGGCGTTAGCCAGGACTTCAACCGGCTTAAAGAGATG 720
QY 722 CAGCTCCAGCAGCTTCAGTCAACCTGCACCTGAGGACCATGTTTC 769
Db 721 CAGCTCCAGCAGCTTCAGTCAACCTGCACCTGAGGACCATGTTTC 768

RESULT 12
AAA88547
ID AAA88547 standard; DNA; 648 BP.
AC AAA88547;
XX
XX 22-JAN-2001 (first entry)
XX Mouse interleukin-B60 (IL-B60) gene.
XX
XX Interleukin-B60; IL-B60; mouse; cytokine; cytokine-like factor-1;
XX haematopoietic; inflammation; antiinflammatory; autoimmune disease;
XX therapy; ds.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 1..648
XX FT /*tag= a
XX FT sig_peptide 1..51
XX FT /*tag= b
XX FT mat_peptide 52..645
XX FT /*tag= c
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XX WO2000053631-A1.
XX
XX 14-SEP-2000.
XX
XX 09-MAR-2000; 2000WO-US006182.
XX
XX 11-MAR-1999; 99US-00267901.
XX (SCHE ) SCHERING CORP.
XX
XX Oppmann B, Timans JC, Kastelein RA, Bazan JF;
```

XX WPI; 2000-587426/55.
DR P-PSDB; AAB19587.

XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
PT polypeptides, and nucleic acids, useful in research, diagnosis and for
PT treating inflammatory and autoimmune disorders.

XX Claim 17; Page 17; 97pp; English.

XX The present sequence is that of DNA encoding mouse interleukin-B60 (IL-B60, see AAB19587), a novel, small soluble cytokine-like protein of 215 amino acids that exhibits structural motifs characteristic of a member of the long chain cytokines, and which shows homology to granulocyte colony stimulating factor and interleukin-6. IL-60B may have either stimulatory or inhibitory effects on haematopoietic cells, including e.g. lymphoid cells, such as T-cells, B-cells, natural killer cells, macrophages, dendritic cells, haematopoietic progenitors, etc. Methods are provided for modulating the physiology or development of a cell or tissue culture cells by contacting the cell with an agonist or antagonist of IL-B60 or an agonist of antagonist of a complex of mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see AAB19588). The IL-B60/CLF-1 cytokine serves as a key physiological factor in motor neuron development and regeneration. IL-60B, its agonists and antagonists may be used to treat inflammatory or autoimmune disorders and also for drug screening

XX Sequence 648 BP; 130 A; 217 C; 170 G; 131 T; 0 U; 0 Other;

Query Match 78.9%; Score 646.4; DB 3; Length 648;
Best Local Similarity 99.8%; Pred. No. 2.8e-151;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 125 ATGTTAGCTTGCTGCTATGACGGTGTGGGACCTCCCTGACGTGCCAGTCCAGCTCTTATTCGC 184

Db 1 ATGTTAGCTTGCTGCTATGACGGTGTGGGACCTCCCTGACGTGCCAGTCCAGCTCTTATTCGC 60

QY 185 ACAGGAGATCCAGGGCCCTGGCCCTCCATCCAGAAAACCTATGACTCACCCGCTACCTG 244

Db 61 ACAGGAGATCCAGGGCCCTGGCCCTCCATCCAGAAAACCTATGACTCACCCGCTACCTG 120

QY 245 GAGCATCACTCCGAGCTTAGCTGGGACCTACCTGACCTGACCTGGGGCCCCCTTTCAC 304

Db 121 GAGCATCACTCCGAGCTTAGCTGGGACCTACCTGACCTGACCTGGGGCCCCCTTTCAC 180

QY 305 GAGCTGACTTCAATCTCTCTGACTGGGGGCGAGAACTCTGCCAGGSCCAAGCTCAAC 364

Db 181 GAGCTGACTTCAATCTCTCTGACTGGGGGCGAGAACTCTGCCAGGSCCAAGCTCAAC 240

QY 365 TTGGAAGTGTGGGAGCCCTCAATGACAGGCTGGGGCTGACCCAGAACTATGAGGCTAC 424

Db 241 TTGGAAGTGTGGGAGCCCTCAATGACAGGCTGGGGCTGACCCAGAACTATGAGGCTAC 300

QY 425 AGTCACCTCTCTGTTACTTGGTGGCCCTCAACCGCTCAGGCTGCCACAGCTGAATCCGA 484

Db 301 AGTCACCTCTCTGTTACTTGGTGGCCCTCAACCGCTCAGGCTGCCACAGCTGAATCCGA 360

QY 485 CBTAGCTGGCCCACTTCTGTACAGCCTTCCAGGCGCTGCTGGGAGCATTCAGGCTGC 544

Db 361 CBTAGCTGGCCCACTTCTGTACAGCCTTCCAGGCGCTGCTGGGAGCATTCAGGCTGC 420

QY 545 ATGGGAGCTTGGCTTACCCACTGGCCCGAGCTCTGCCAGGAGCTGAGCCCTGGGCC 604

Db 421 ATGGGAGCTTGGCTTACCCACTGGCCCGAGCTCTGCCAGGAGCTGAGCCCTGGGCC 480

QY 605 CCTGGCCCTGGCCCACTGACTTCTCCAGAAAGATGATGACTTCTGGCTGTGAAGGAG 664

Db 481 CCTGGCCCTGGCCCACTGACTTCTCCAGAAAGATGATGACTTCTGGCTGTGAAGGAG 540

QY 665 CTGCAGACTGCTGCTATGGCTTACCCAGGAGCTTCAACCGCTTAAAGAGAGATGAG 724

Db 541 CTGCAGACTGCTGCTATGGCTTACCCAGGAGCTTCAACCGCTTAAAGAGAGATGAG 600

QY 725 CTTCCAGCAGCTTCAGTCAACCTGCACTTGGAGGACATGTTTCTGA 772

/product= "Human mature cardiotrophin-like cytokine (CLC) protein"

WO200127157-A1.

19-APR-2001.

06-OCT-2000; 2000WO-AU001216.

08-OCT-1999; 99AU-00003327.

12-MAY-2000; 2000AU-00007489.

(AMRA-) AMRAD OPERATIONS PTY LTD.

Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ, Nakata Y, Hasegawa M;

WPI; 2001-281978/29.

P-PSDB; RAE00828.

New biologically active complex comprising NR6 and cardiotrophin-like-cytokine, for facilitating proliferation, differentiation and/or survival of a cell.

Claim 31; Page 112-114; 123pp; English.

The present invention relates to a biologically active complex comprising a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC). The complex is useful in the manufacture of a medicament for the treatment and/or prophylaxis of a subject, as it is involved in facilitating proliferation, differentiation and/or survival of a cell. The complex or its components have neurotrophic activity. The present sequence is human cardiotrophin-like cytokine (CLC) cDNA

Sequence 729 BP; 132 A; 261 C; 196 G; 140 T; 0 U; 0 Other;

Query Match 73.3%; Score 600.2; DB 4; Length 729;

Best Local Similarity 91.6%; Pred. No. 9.4e-140;

Matches 635; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 91 CCCATGACCTCGACAGGAGACTCGTGGGATGTTAGCTTGCTATGACAGGTGCT 150

Db 7 CCCATGACCTCGACAGGAGACTCGTGGGATGTTAGCTTGCTATGACAGGTGCT 66

QY 151 GTGCACCTCCCTCAGTGCAGCTCTTAATCGACAGGAGATCCAGGCCCTGGCCCTC 210

Db 67 CTGCGACCTCCTGCACTGCAGCTCTTAATCGACAGGAGATCCAGGCCCTGGCCCTC 126

QY 211 CATCCAGAAACCTATGACCTACCCGCTACCTGGAGCATCAACTCCGACGCTTAGCTGG 270

Db 127 CATCCAGAAACCTATGACCTACCCGCTACCTGGAGCATCAACTCCGACGCTTAGCTGG 186

QY 271 GACCTACCTGACCTACCTGGGCCCCCTTTCAAGAGCCTGACTTCAATCTCTCGACT 330

Db 187 GACCTATCTGACCTACCTGGGCCCCCTTTCAAGAGCCTGACTTCAATCTCTCGACT 246

QY 331 GGGGCGAGAACTCTGCCCGGCGCAGCTCAACTTGGAACTGTGGCAAGCCTCAATGA 390

Db 247 GGGGCGAGAACTCTGCCCGGCGCAGCTCAACTTGGAACTGTGGCAAGCCTCAATGA 306

QY 391 CAGGCTCGGCTGACCCAGAACTATGAGGCGTACGTCACCTCCTGTGTACTTGGGTGG 450

Db 307 CAAATCTCGGCTGACCCAGAACTATGAGGCGTACGTCACCTCCTGTGTACTTGGGTGG 366

QY 451 CCTCAACGCTCAGCTGCCAGCTGAACCTCCAGCTGAGCTGGCCCACTTCGTACCCAG 510

Db 367 CCTCAACGCTCAGCTGCCAGCTGAGCTGGCCCGAGCTGGCCCACTTCGTACCCAG 426

QY 511 CCTCCAGGCTGCTGGGAGCAATTCAGGTGTTCATGGGACGCTTGGCTACCCACTGCC 570

Db 427 CCTCCAGGCTGCTGGGAGCAATTCAGGTGTTCATGGGAGCTTGGGCTACCCACTGCC 486

QY 571 CCAGCTCTGCCAGGACTGAGCCAGCTGGGCCCCCTGGCCCTGCCACAGTACTCT 630

Db 487 CCAGCGCTGCTGGGACTGAAACCCACTTGGACTCTGGCCCTGCCACAGTACTCT 546

QY 631 CCAGAAGATGATGACTTCTGGCTCTGAAGAGCTGAGAGCTGGCTATGCGGTTCAGC 690

Db 547 CCAGAAGATGAGAGCTTCTGGCTCTGAAGAGCTGAGAGCTGGCTATGCGGTTCAGC 606

QY 691 CAAGGACTTCAACCGGCTTAAGAAGAAGATGAGAGCTCCAGAGCTTCACTCAGCTTCA 750

Db 607 CAAGGACTTCAACCGGCTCAAGAAGAAGATGAGAGCTCCAGAGCTTCACTCAGCTTCA 666

QY 751 CTTGGAGGACATGTTCTTCTGACCTTGACCTT 783

Db 667 CTTGGAGGACATGTTCTTCTGACCTTCTGACCTT 699

RESULT 15

AAKS1548

ID AAKS1548 standard; cDNA; 1008 BP.

XX AC AAKS1548;

XX AC

DT 06-NOV-2001 (first entry)

XX DE Human polynucleotide SEQ ID NO 93.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy; KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis; KW tissue growth factor; immunomodulatory; cancer; leukaemia; KW nervous system disorder; arthritis; inflammation; ss.

XX OS Homo sapiens.

XX PN WO200157190-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US004098.

XX PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663581.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

XX (HYSE-) HYSEQ INC.

XX PA Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Xue AJ, Yang Y, Wehrman T, Goodrich R;

XX PI WPI; 2001-476283/51.

XX DR P-PSDB; AAM78415.

XX PT Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.

XX PS Claim 1; Page 711-712; 622ipp; English.

XX CC The invention relates to polynucleotides (AAKS1456-AAKS3435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAKS2581), 2111

CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 1008 BP; 183 A; 374 C; 247 G; 204 T; 0 U; 0 Other;

Query Match		71.2%;	Score 583.2;	DB 4;	Length 1008;
Best Local Similarity		90.8%;	Pred. No. 1.8e-135;		
Matches 621;		Conservative 0;	Mismatches 63;	Indels 0;	Gaps 0;
QY	100	CCTCGAGCAGGGGACTCGTGGGGATGTAGCTTGCCTATGTCACGGTGTGTGGCACCT	159		
DB	296	CCTGCCACAGGGGACTCGTGGGGATGTAGCTTGCCTATGTCACGGTGTGTGGCACCT	355		
QY	160	CCCTCAGTGCAGCTCTTAATCGACAGAGATCCAGGCCCTGGCCCCCTCCATCCAGAA	219		
DB	356	CCCTCAGTGCAGCTCTTAATCGACAGAGATCCAGGCCCTGGCCCCCTCCATCCAGAA	415		
QY	220	AACTATGACCTCACCGCTACCTGGAGCATCAACTCCGAGCTTAGCTGGGAGCTACCT	279		
DB	416	AACTATGACCTCACCGCTACCTGGAGCATCAACTCCGAGCTTAGCTGGGAGCTACCT	475		
QY	280	GAACTACCTGGGGCCCCCTTTCAACGAGCCTGACTTCAATCCTCTCGACTGGGGGAGA	339		
DB	476	GAACTACCTGGGGCCCCCTTTCAACGAGCCTGACTTCAATCCTCTCGACTGGGGGAGA	535		
QY	340	AACTCTGCCAGGGCCACGGTCAACTTGAAGTGTGGGAGGCTCAATGACAGGCTGCG	399		
DB	536	AACTCTGCCAGGGCCACGGTCAACTTGAAGTGTGGGAGGCTCAATGACAGGCTGCG	595		
QY	400	GCTGACCCAGAACTATGAGCGCTACAGTCACCTCCTGTGTACTTTCGCTGGCCTCAACCG	459		
DB	596	GCTGACCCAGAACTATGAGCGCTACAGTCACCTCCTGTGTACTTTCGCTGGCCTCAACCG	655		
QY	460	TCAGGCTGCCACAGCTGAATCCGAGTGTAGCTGGCCCTTCTGTACAGGCTCCAGGG	519		
DB	656	TCAGGCTGCCACAGCTGAATCCGAGTGTAGCTGGCCCTTCTGTACAGGCTCCAGGG	715		
QY	520	CCTGCTGGGCAGCATTTGAGGTGTATGGCGAGCTTGGCTACCCACTGCCCCAGCCTCT	579		
DB	716	CCTGCTGGGCAGCATTTGAGGTGTATGGCGAGCTTGGCTACCCACTGCCCCAGCCTCT	775		
QY	580	GCCAGGACTGAGCAGCCTGGGGCCCTGGCCCTGCCACAGTGTACTTCTCCAGAGAT	639		
DB	776	GCCAGGACTGAGCAGCCTGGGGCCCTGGCCCTGCCACAGTGTACTTCTCCAGAGAT	835		
QY	640	GGATGACTTCTGGCTGCAAGGAGTGCAGACCTGGCTATGGCGTTTCAGGCCAAGGACTT	699		
DB	836	GGATGACTTCTGGCTGCAAGGAGTGCAGACCTGGCTATGGCGTTTCAGGCCAAGGACTT	895		
QY	700	CAACCGGCTTAAGAGAGATGACGCTCCAGCAGCTTCAAGTCAACCTGCACTTGGAGGC	759		
DB	896	CAACCGGCTTAAGAGAGATGACGCTCCAGCAGCTTCAAGTCAACCTGCACTTGGAGGC	955		
QY	760	ACATGCTTCTGACCTTCAACCT 783			
DB	956	TCATGGCTTCTGACTTCTGACCTT 979			

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Job time : 282.413 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 16:49:33 ; Search time 473.586 Seconds
(without alignments)
8485.292 Million cell updates/sec

Title: US-09-931-704-4

Perfect score: 819
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 245330834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:

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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
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17: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	819	100.0	819	9	US-09-931-704-4
2	669.4	81.7	797	9	Sequence 4, Appli
3	660	80.6	768	13	Sequence 1, Appli
4	627	76.6	1710	15	Sequence 607, App
5	577	70.5	968	13	Sequence 1, Appli
6	429.6	52.5	5087	9	Sequence 916, App
7	419.8	51.3	495	9	Sequence 3, Appli
8	299.2	36.5	492	9	Sequence 23175, A
9	236	28.8	283	9	Sequence 6462, Ap
10	158	19.3	809	13	Sequence 75, Appl
11	158	19.3	809	16	Sequence 134702,
12	65	7.9	65	10	Sequence 134702,
13	52	6.3	396	15	Sequence 29446, A
14	46	5.6	951	15	Sequence 7, Appli
					Sequence 1403, Ap

5.6 9025608 15 US-10-156-761-1
5.2 1578 9 US-09-880-107-3440
5.0 2750 16 US-10-108-260A-1682
5.0 3208 10 US-02-814-353-19617
5.0 34096 13 US-10-087-192-952
4.9 500 13 US-10-027-632-287452
4.9 500 16 US-10-027-632-287452
4.9 594 13 US-10-142-426-10
4.9 594 15 US-10-123-155-10
4.9 594 15 US-10-146-731-10
4.9 594 15 US-10-140-472-10
4.9 594 15 US-10-141-761-10
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4.9 594 16 US-10-137-871-10
4.9 594 16 US-10-140-923-10
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4.9 594 16 US-10-140-864-10
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4.8 500 13 US-10-027-632-287450
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4.8 500 16 US-10-027-632-287449
4.8 500 16 US-10-027-632-287450
4.8 500 16 US-10-027-632-287451
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4.8 1180 17 US-10-437-963-24598
4.8 867 13 US-10-142-426-20
4.8 867 15 US-10-123-155-20
4.8 867 15 US-10-146-731-20
4.8 867 15 US-10-140-472-20

ALIGNMENTS

RESULT 1

US-09-931-704-4
; Sequence 4, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Methods and Compositions for Treating Ige-Related Disease Using N
; FILE OF INVENTION: Inhibitors
; FILE REFERENCE: A-695
; CURRENT APPLICATION NUMBER: US/09/931,704
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (95)..(769)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (176)..()
; OTHER INFORMATION:
; NAME/KEY: mat_peptid
; LOCATION: (176)..(769)
; OTHER INFORMATION:
; NAME/KEY: sig_peptide
; LOCATION: (95)..(175)
; OTHER INFORMATION:
US-09-931-704-4

Query Match 100.0%; Score 819; DB 9; Length 819;
Best Local Similarity 100.0%; Pred No. 2,4e-225; Indels 0; Gaps 0;
Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 589 TGAGCCAGCCTGGGCCCCCTGGCCCTGCCACAGTGAATCTCTCCAGAGATGGATGACTT 648
Db |||||
QY 540 TGAACCCACTTGGACTCTCTGGCCCTGCCACAGTGAATCTCTCCAGAGATGGAGACTT 599
Db |||||
QY 649 CTGGCTGCTGAAGGAGCTGCAGACCTGGCTATATGGGCTTTCAGCAAGAGACTTCAACCGGCT 708
Db |||||
QY 600 CTGGCTGCTGAAGGAGCTGCAGACCTGGCTATATGGGCTTTCAGCAAGAGACTTCAACCGGCT 659
Db |||||
QY 709 TGAAGAAGATGCGAGCCTCCAGAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
Db |||||
QY 660 CAAGAAGAAGATGCGAGCCTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719
Db |||||
QY 769 CTGACCTCTGACCT 783
Db |||||
QY 720 CTGACTTCTGACCTT 734
Db |||||

RESULT 5

US-10-276-774-916
; Sequence 916, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 916
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-916

Query Match 70.5%; Score 577; DB 13; Length 968;
Best Local Similarity 91.1%; Pred. No. 9e-156;
Matches 613; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 100 CTTCCAGAGAGGAGCTCTGGGGATGTTAGTTCCTATGACAGGTGCTGTGGACCT 159
Db |||||
QY 296 CTTCCAGAGAGGAGCTCTGGGGATGTTAGTTCCTATGACAGGTGCTGTGGACCT 355
Db |||||
QY 160 CTTCCAGAGAGGAGCTCTGGGGATGTTAGTTCCTATGACAGGTGCTGTGGACCT 219
Db |||||
QY 356 CTTCCAGAGAGGAGCTCTGGGGATGTTAGTTCCTATGACAGGTGCTGTGGACCT 415
Db |||||
QY 220 AACCTATGACCTACCCGCTTCTGAGGATCAATTCGCGAGCTTGTGGACCTACCT 279
Db |||||
QY 416 AACCTATGACCTACCCGCTTCTGAGGATCAATTCGCGAGCTTGTGGACCTACCT 475
Db |||||
QY 280 GAATACCTGGGGCCCTTCAACGAGCTGACTTCAATCTCTGCTGCTGCTGCTGCTGCT 339
Db |||||
QY 476 GAATACCTGGGGCCCTTCAACGAGCTGACTTCAATCTCTGCTGCTGCTGCTGCTGCT 535
Db |||||
QY 340 AACCTGCCCCAGGAGCCAGCTTCAATTCGGAAGTGGGAGCTTCAATGACAGGCTGCG 399
Db |||||
QY 536 GACTCTGCCAGGAGGAGCTTGTGAGGAGTGGGAGGAGCTTCAATGACAACTGCG 595
Db |||||
QY 400 GCTGACCCAGAACTATGAGCGCTACAGTCACTCTCTGTTTACTTGGCTGAGCTCAACCG 459
Db |||||
QY 596 GCTGACCCAGAACTATGAGCGCTTACAGCCACTTCTGTTTACTTGGCTGAGCTCAACCG 655
Db |||||
QY 460 TCAGGCTGCGACAGCTGAACTCCGAGCTAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 519
Db |||||
QY 656 TCAGGCTGCGACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 715
Db |||||

QY 520 CTTGCTGGGAGCATTGCGAGTCTCATGGAGCGCTTGGCTACCCAGTCCCCAGCTCT 579
Db |||||
QY 716 CTTGCTGGGAGCATTGCGAGTCTCATGGAGCGCTTGGCTACCCAGTCCCCAGCTCT 775
Db |||||
QY 580 GCGAGGAGCTGAGCCAGCCTTGGGCCCTGGCCCTGCCACAGTGAATCTCTCCAGAGAT 639
Db |||||
QY 776 GCTTGGGAGCTGAAACCCACTTGGACTCTGGCCCTGCCACAGTGAATCTCTCCAGAGAT 835
Db |||||
QY 640 GGATGACTTCTGCTGCTGAGGAGCTGCGAGCTTATGGCTATGGCTTTCAGCCAGGACTT 699
Db |||||
QY 836 GGAGGACTTCTGCTGCTGAGGAGCTGCGAGCTTATGGCTATGGCTTTCAGCCAGGACTT 895
Db |||||
QY 700 CAACCCGCTTGAAGAAGATGCGAGCTTCCAGAGCTTTCAGTCACTGAGCTTGGAGC 759
Db |||||
QY 896 CAACCCGCTTGAAGAAGATGCGAGCTTCCAGAGCTTTCAGTCACTGAGCTTGGAGC 955
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QY 760 ACATGGTTTCTGA 772
Db |||||
QY 956 TCATGGCTTCTGA 968
Db |||||

RESULT 6

US-09-931-704-3
; Sequence 3, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Methods and Compositions for Treating Ige-Related Disease Using NT
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: A-695
; CURRENT APPLICATION NUMBER: US/09/931,704
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5087
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (137)..(138)
; OTHER INFORMATION: product = "INTERVENING UNSEQUENCED REGION OF >1KB"
US-09-931-704-3

Query Match 52.5%; Score 429.6; DB 9; Length 5087;
Best Local Similarity 90.4%; Pred. No. 2.7e-113;
Matches 459; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 276 ACCTGAACCTACCTGGGGCCCCCTTCAAGAGCTGACTTCAATCTCTGCTGCTGCTGCTGCT 335
Db |||||
QY 3363 AGCTGAACCTACCTGGGGCCCCCTTCAAGAGCTGACTTCAATCTCTGCTGCTGCTGCTGCT 3422
Db |||||
QY 336 CAGAAACTCTGCCCCAGGGCCACGGTCAACTTGAAGTGGGAGAGCTTCAATGACAGC 395
Db |||||
QY 3423 CAGAGACTCTGCCAGGGCCACCTTGTGACTTGGAGGTGGGAGAGCTTCAATGACAAAC 3482
Db |||||
QY 396 TGGGCTGAGCCAGAACTATGAGCGCTGAGCTACAGTCACTCTGTTTACTTGGCTGCTGCT 455
Db |||||
QY 3483 TGGGCTGAGCCAGAACTATGAGCGCTGAGCTACAGTCACTCTGTTTACTTGGCTGCTGCT 3542
Db |||||
QY 456 ACCGTGAGGCTGCGACAGCTGAACTCCGAGCTAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 515
Db |||||
QY 3543 ACCGTGAGGCTGCGACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 3602
Db |||||
QY 516 AGGCTGCTGGGAGAGCTTGAAGTGTATGAGCGAGCTTGGCTACCCAGTCCCCAGC 575
Db |||||
QY 3603 AGGCTGCTGGGAGAGCTTGAAGTGTATGAGCGAGCTTGGCTACCCAGTCCCCAGC 3662
Db |||||
QY 576 CTCTGCGAGGAGCTGAGCCAGCTTGGGCCCTTGGGCCCTTGGGCCCTTGGGCCCTTGGGCCCT 635
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QY 3663 CTCTGCGAGGAGCTGAGCCAGCTTGAAGTGTATGAGCGAGCTTGGCTACCCAGTCCCCAGC 3722
Db |||||

QY 636 AGATGATGACTTGGCTGCTGAAGGAGCTGAGAGCTGGCTATGGCTTACGCAAGG 695
DB 3723 AGATGAGCACTTCTGCTGCTGAGGAGCTGAGAGCTGGCTTGGCTTGGCAAGG 3782
QY 696 ACTTCAACCGGCTTAAGAAGAAGTGCAGCTCCAGCAGCTTCAGTCAACCTGACTTGG 755
DB 3783 ACTTCAACCGGCTCAAGAAGAAGTGCAGCTCCAGCAGCTGAGTCAACCTGCACTGG 3842
QY 756 AGGCATGCTTCTGACCTTGCACCT 783
DB 3843 GGGCTCATGGCTTCTGACTTGCACCT 3870

RESULT 7
US-09-864-761-23175/c
; Sequence 23175, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-x-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23175
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005849.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: SWISSPROT HIT: Q63086, EVALUE 8.00e-03
; OTHER INFORMATION: NT HIT: g111439486, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: A1752561.1, EVALUE 0.00e+00
US-09-864-761-23175

Query Match 51.3%; Score 419.8; DB 9; Length 495;
Best Local Similarity 90.5%; Pred. No. 1.3e-110;
Matches 448; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 278 CTGAACCTGCGGGCCCGCCCTTTCAACGAGCTGACTTCAATCTCTCCCTGGCTGGGGCA 337
DB 495 CTGAACCTGCGGGCCCGCCCTTTCAACGAGCTGACTTCAACCTCTCCCGCTGGGGCA 436
QY 338 GAAACTCTGCCCGAGGCGCACGGTCAACTTGAAGTGTGGCGGCGCAAGCTCAATGACAGGCTG 397
DB 435 AAGACTCTGCCCGAGGCGCACCTGTTGACTTGGAGGTGTGGCGAAGCTCAATGACAACTG 376
QY 398 CGGCTGACCGAAGTATGAGGCGTACAGTACCTCTCTGTGTACTTGGTGGCTCAAC 457
DB 375 CGGCTGACCGAAGTATGAGGCGCTTACAGGCGCTTCTGTGTACTTGGTGGCTCAAC 316
QY 458 CGTCAAGCTGCCACAGCTGAACCTCGAGCTGAGCTGGCGGCCCTCTGTACCAAGCTCCAG 517
DB 315 CGTCAAGCTGCCACCTGCTGAGCTGGCGGCGCTGGCGGCGCTTGTGACCAAGCTCCAG 256
QY 518 GGCCTGTGGCGAGCAATTGAGGTGTATGCGAGCGCTTGGCTACCCACTGCCCGAGCT 577
DB 255 GGCCTGTGGCGAGCAATTGCGGGCGCTCATGGCAGCTCTGGGCTACCCACTGCCCGAGCG 196
QY 578 CTGCCAGGAGCTGAGCGAGCTGGCGGCCCTGGCGGCCCTGCAGAGCTTCTCTCCAGAG 637
DB 195 CTGCTGGAGCTGAACCACTTGGACTCTTGCCCTGCCAGAGCTGCGAGACCTGGCTGGCGCAAG 136
QY 638 ATGGATGACTTCTGGCTGTCTGAAGGAGCTGCAGACCTGGCTATGGCTTACGCCAAGGAC 697
DB 135 ATGGAGCACTTCTGGCTGTCTGAAGGAGCTGCAGACCTGGCTGTGGCGCTGGCGCAAGGAC 76
QY 698 TTCAACCGGCTTAAGAAGAAGTGCAGGCTCCAGGAGCTTCAATGACCTGAGCTGGAG 757
DB 75 TTCAACCGGCTCAAGAAGAAGTGCAGGCTCCAGGAGCTTCAATGACCTGAGCTGGAG 16
QY 758 GCACATGGTTTCTGA 772
DB 15 GCTCATGCTTCTGA 1

RESULT 8
US-09-864-761-6462/c
; Sequence 6462, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03


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; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134702
; LENGTH: 809
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-134702

Query Match      19.3%; Score 158; DB 13; Length 809;
Best Local Similarity 88.5%; Pred. No. 2.4e-35;
Matches 170; Conservative 1; Mismatches 21; Indels 0; Gaps 0;

QY 100 CCTCCGAGCGGACGCTGCGGGGATGTTAGCTTGCTATGACGCGTGTGGCACCT 159
Db 46 CCTCCACACAGGACGCTGCGGGGATGTTAGCTTGCTATGACGCGTGTGGCACCT 105

QY 160 CCTCGAGTGCAGCTCTTAATCGCACAGGAGATCCAGGCCCTGGCCCTCCATCCAGAA 219
Db 106 CCTCGAGTGCAGCTCTTAATCGCACAGGAGATCCAGGCCCTGGCCCTCCATCCAGAA 165

QY 220 AACCTATGACCTACCGCTACCTGGAGCATCAACTCCGACGCTTAGCTGGACCTACCT 279
Db 166 AACCTATGACCTACCGCTACCTGGAGCACCACCACTCCGACGCTTGGCTGGACCTATGT 225

QY 280 GAACCTACCTGGG 291
Db 226 GAGTATCCAGCG 237

Query Match      19.3%; Score 158; DB 16; Length 809;
Best Local Similarity 88.5%; Pred. No. 2.4e-35;
Matches 170; Conservative 1; Mismatches 21; Indels 0; Gaps 0;

QY 100 CCTCCGAGCGGACGCTGCGGGGATGTTAGCTTGCTATGACGCGTGTGGCACCT 159
Db 46 CCTCCACACAGGACGCTGCGGGGATGTTAGCTTGCTATGACGCGTGTGGCACCT 105

QY 160 CCTCGAGTGCAGCTCTTAATCGCACAGGAGATCCAGGCCCTGGCCCTCCATCCAGAA 219
Db 106 CCTCGAGTGCAGCTCTTAATCGCACAGGAGATCCAGGCCCTGGCCCTCCATCCAGAA 165

QY 220 AACCTATGACCTACCGCTACCTGGAGCATCAACTCCGACGCTTAGCTGGACCTACCT 279
Db 166 AACCTATGACCTACCGCTACCTGGAGCACCACCACTCCGACGCTTGGCTGGACCTATGT 225

QY 280 GAACCTACCTGGG 291
Db 226 GAGTATCCAGCG 237

RESULT 11
US-10-027-632-134702
; Sequence 134702, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134702
; LENGTH: 809
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-134702

Query Match      19.3%; Score 158; DB 16; Length 809;
Best Local Similarity 88.5%; Pred. No. 2.4e-35;
Matches 170; Conservative 1; Mismatches 21; Indels 0; Gaps 0;

QY 100 CCTCCGAGCGGACGCTGCGGGGATGTTAGCTTGCTATGACGCGTGTGGCACCT 159
Db 46 CCTCCACACAGGACGCTGCGGGGATGTTAGCTTGCTATGACGCGTGTGGCACCT 105
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QY 160 CCTCGAGTGCAGCTCTTAATCGCACAGGAGATCCAGGCCCTGGCCCTCCATCCAGAA 219
Db 106 CCTCGAGTGCAGCTCTTAATCGCACAGGAGATCCAGGCCCTGGCCCTCCATCCAGAA 165

QY 220 AACCTATGACCTACCGCTACCTGGAGCATCAACTCCGACGCTTAGCTGGACCTACCT 279
Db 166 AACCTATGACCTACCGCTACCTGGAGCACCACCACTCCGACGCTTGGCTGGACCTATGT 225

QY 280 GAACCTACCTGGG 291
Db 226 GAGTATCCAGCG 237

RESULT 12
US-09-908-975-29446
; Sequence 29446, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29446
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-908-975-29446

Query Match      7.9%; Score 65; DB 10; Length 65;
Best Local Similarity 100.0%; Pred. No. 9.2e-09;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 CTGAAGGAGCTGCAGACCTGCTATGGCTTTCAGCAAGGACTTCAACCGGCTTAAGAAG 715
Db 1 CTGAAGGAGCTGCAGACCTGCTATGGCTTTCAGCAAGGACTTCAACCGGCTTAAGAAG 60

QY 716 AAGAT 720
Db 61 AAGAT 65

RESULT 13
US-10-212-793-7
; Sequence 7, Application US/10212793
; Publication No. US20030087395A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
; FILE REFERENCE: PF385D1C1
; CURRENT APPLICATION NUMBER: US/10/212,793
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 09/438,299
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/106,182
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: US 60/051,311
; PRIOR FILING DATE: 1997-06-30
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 7
; LENGTH: 396
; TYPE: DNA
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ORGANISM: homo sapiens
 FEATURE:
 NAME/KEY: Site
 LOCATION: (199)
 OTHER INFORMATION: n equals any nucleotide
 FEATURE:
 NAME/KEY: Site
 LOCATION: (293)
 OTHER INFORMATION: n equals any nucleotide
 FEATURE:
 NAME/KEY: Site
 LOCATION: (306)
 OTHER INFORMATION: n equals any nucleotide
 FEATURE:
 NAME/KEY: Site
 LOCATION: (360)
 OTHER INFORMATION: n equals any nucleotide
 FEATURE:
 NAME/KEY: Site
 LOCATION: (371)
 OTHER INFORMATION: n equals any nucleotide
 FEATURE:
 NAME/KEY: Site
 LOCATION: (377)
 OTHER INFORMATION: n equals any nucleotide
 FEATURE:
 NAME/KEY: Site
 LOCATION: (383)
 OTHER INFORMATION: n equals any nucleotide
 US-10-212-793-7

Query Match 6.3%; Score 52; DB 15; Length 396;
 Best Local Similarity 85.3%; Pred. No. 6.5e-05;
 Matches 58; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 716 AGATGACCCCTCCAGCAGCTTCAGTCCACCTGACCTGGAGGACATGTTCTGACCT 775
 DB 4 ACAGGACAGCTCCAGCAGCTGACGACCTGACCTGACCTGGGGGCTCATGCTTCAACT 63
 QY 776 CTGACCT 783
 DB 64 CTGACCT 71

RESULT 14
 US-10-156-761-1403/c
 ; Sequence 1403, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 1403
 ; LENGTH: 951
 ; TYPE: DNA
 ; ORGANISM: Streptomyces avermitilis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(951)
 ; US-10-156-761-1403

Query Match 5.6%; Score 46; DB 15; Length 951;
 Best Local Similarity 52.0%; Pred. No. 0.0039;
 Matches 103; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 430 CTTCTGTGTACTTGGTGGCTCAACCGTCAAGGTGCCAGCTGAACTCCGACGTAG 489
 DB CTTCTGTGTACTTGGTGGCTCAACCGTCAAGGTGCCAGCTGAACTCCGACGTAG 503
 QY 490 CTTGGGCCACTTCTGTACAGCTCCAGGCTGCTGGGAGCATTGACGGTGTATGGC 549
 DB TCTCGCCACAGCTTCGCCCCAGTCCGACGAGTGGTCCGTCACCTGTCGCGGTCCA 443
 QY 550 GACGCTTGGCTACCCACTGCCCCAGCTCTGCCAGGACTGAGCCAGCTGGGGCCCCCTGG 609
 DB 442 GAGCCATGTACGCTTCTGGGCCCATCAGCGGACGCTGAGCGAGCTCCGCTCCCC 383
 QY 610 CCTGCCCCACAGTACTT 627
 DB 382 ACCTACCTGCCCGTCTT 365

RESULT 15
 US-10-156-761-1
 ; Sequence 1, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 1
 ; LENGTH: 9025608
 ; TYPE: DNA
 ; ORGANISM: Streptomyces avermitilis
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (4187715)
 ; OTHER INFORMATION: a, t, c, g, other or unknown
 US-10-156-761-1

Query Match 5.6%; Score 46; DB 15; Length 9025608;
 Best Local Similarity 52.0%; Pred. No. 0.015;
 Matches 103; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 430 CTTCTGTGTACTTGGTGGCTCAACCGTCAAGGTGCCAGCTGAACTCCGACGTAG 489
 DB 1746625 CTTCCAGCGTGAACAGCCAGCGCCGACCGTCCCGGCCACCGTGGTGGTCA 1746684
 QY 490 CTTGGGCCACTTCTGTACAGCTCCAGGCTGCTGGGAGCATTGACGGTGTATGGC 549
 DB 1746685 TCTCGCCACAGCTTCGCCCCAGTCCGACGAGTGGTCCGTCACCTGTCGCGGTCCA 1746744
 QY 550 GACGCTTGGCTACCCACTGCCCCAGCTCTGCCAGGACTGAGCCAGCTGGGGCCCCCTGG 609
 DB 1746745 GAGCCATGTACGCTTCTGGGCCCATCAGCGGACGCTGAGCGAGCTCCGCTCCCC 1746804
 QY 610 CCTGCCCCACAGTACTT 627
 DB 1746805 ACCTACCTGCCCGTCTT 1746822

Search completed: August 16, 2004, 10:40:19
Job time : 485.586 secs

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OM nucleic - nucleic search, using sw model

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Title: US-09-931-704-4

Perfect score: 819

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 692709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	819	100.0	819	1	US-08-792-019B-4
2	819	100.0	819	3	US-08-988-819-4
3	819	100.0	819	3	US-08-988-819-4
4	669.4	81.7	797	1	US-08-792-019B-1
5	669.4	81.7	797	3	US-08-988-819-1
6	669.4	81.7	797	3	US-08-988-819-1
7	627	76.6	1710	3	US-09-106-182-1
8	429.6	52.5	5087	1	US-08-792-019B-3
9	429.6	52.5	5087	3	US-08-988-819-3
10	429.6	52.5	5087	3	US-08-988-819-3
11	52	6.3	396	3	US-09-106-182-7
12	43.2	5.3	6803	3	US-08-665-259-19
13	43.2	5.3	6803	3	US-08-665-259-19
14	42.4	5.2	1642	2	US-08-665-037-1
15	42.4	5.2	1642	2	US-08-665-067-1
16	42.4	5.2	1642	2	US-08-732-870-1
17	38.4	4.7	68750	3	US-09-335-409-1
18	38.4	4.7	68750	3	US-09-568-102-1
19	38.4	4.7	68750	4	US-09-567-969-1
20	38.4	4.7	68750	4	US-09-568-480-1
21	38.4	4.7	68750	4	US-09-568-486-1
22	38.4	4.7	68750	4	US-09-568-472-1
23	38.4	4.7	68750	4	US-09-567-899-1
24	37.8	4.6	364	4	US-09-621-976-17202
25	37	4.5	789	4	US-09-252-991A-5788
26	37	4.5	957	4	US-09-252-991A-5803
27	37	4.5	1248	4	US-09-252-991A-5821

Sequence 599, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 759, Appl
Sequence 203, Appl
Sequence 17, Appl
Sequence 2876, Ap
Sequence 3182, Ap
Sequence 2687, Ap
Sequence 2859, Ap
Sequence 127, App
Sequence 2659, Ap
Sequence 2759, Ap
Sequence 3207, Ap
Sequence 2, Appli
Sequence 1, Appli
Sequence 16566, A
Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-792-019B-4
; Sequence 4, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,019B
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 95..769
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 176..769
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 95..175
US-08-792-019B-4

Query Match 100.0%; Score 819; DB 1; Length 819;
Best Local Similarity 100.0%; Pred. No. 6.5e-208;
Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 541 TGTATGCGGAGCGTGTGGTACCCAGCTGCCCCAGCTTGTCCAGGAGCTGAGCGAGCTG 600
Db 541 TGTATGCGGAGCGTGTGGTACCCAGCTGCCCCAGCTTGTCCAGGAGCTGAGCGAGCTG 600
QY 601 GGCCCTGCGCTGCGGAGCTGCTTCCAGAGATGATGACTTGTGGCTGTGAA 660
Db 601 GGCCCTGCGCTGCGGAGCTGCTTCCAGAGATGATGACTTGTGGCTGTGAA 660
QY 661 GGAGCTGAGAGCTGCGCTTACAGCAAGAGCTTCAACCGGCTTAAAGAGAGAT 720
Db 661 GGAGCTGAGAGCTGCGCTTACAGCAAGAGCTTCAACCGGCTTAAAGAGAGAT 720
QY 721 CGAGCTCCAGAGCTTCAAGTCACTCCAGCTTCCAGAGCAATGGTTCTGAGCTTGAC 780
Db 721 CGAGCTCCAGAGCTTCAAGTCACTCCAGCTTCCAGAGCAATGGTTCTGAGCTTGAC 780
QY 781 CCTTAACCCCCACAGCTTCCAGGCGGAGCTGAGCTGTGCTT 819
Db 781 CCTTAACCCCCACAGCTTCCAGGCGGAGCTGAGCTGTGCTT 819

RESULT 3
US-09-016-534-4
; Sequence 4, Application US/09016534
; Patent No. 6143874
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: ELLIOTT, GARY S.
; APPLICANT: SARMIENTO, ULLA
; APPLICANT: SENALDI, GIORGIO
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/016.534
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/792,019
; APPLICATION NUMBER: 03-FEB-1997
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442B
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 95..769
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 176..769
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 95..175
US-09-016-534-4

Query Match 100.0%; Score 819; DB 3; Length 819;
Best Local Similarity 100.0%; Pred No. 6,5e-208; Mismatches 0; Indels 0; Gaps 0;
Matches 819; Conservative 0;
QY 1 TATTATTAAGCTTCCCGGAGCGCGGCTCGCCCTCCACCTCCGAGAGGAGCTTGGGAGA 60
Db 1 TATTATTAAGCTTCCCGGAGCGCGGCTCGCCCTCCACCTCCGAGAGGAGCTTGGGAGA 60
QY 61 GGAGCG 120
Db 61 GGAGCG 120
QY 121 GGGATGTTAGCTTGGCTATGACGCGTGTGGACCTCCCTCCAGTCCAGTCCAGTCCAGT 180
Db 121 GGGATGTTAGCTTGGCTATGACGCGTGTGGACCTCCCTCCAGTCCAGTCCAGTCCAGT 180
QY 181 TCGCAGAGAGATCCAGGCGCTGGCGCTTCCATCCAGAAACCTATGACCTCACCGGCTA 240
Db 181 TCGCAGAGAGATCCAGGCGCTGGCGCTTCCATCCAGAAACCTATGACCTCACCGGCTA 240
QY 241 CCTGGAGCATCAACTCCGAGCTTATGCTGGGACCTTACCTGGAACCTACCTGGGGCCCCCTTT 300
Db 241 CCTGGAGCATCAACTCCGAGCTTATGCTGGGACCTTACCTGGAACCTACCTGGGGCCCCCTTT 300
QY 301 CAACGAGCTGACTTCAATCTCTCGACTGGGGGAGAACTCTGCCCGAGGCGCACGGT 360
Db 301 CAACGAGCTGACTTCAATCTCTCGACTGGGGGAGAACTCTGCCCGAGGCGCACGGT 360
QY 361 CAACTTGGAAAGTGTGGGAGAGCTCAATCAGAGGCTGGGGCTGACCCAGAACTATGAGGC 420
Db 361 CAACTTGGAAAGTGTGGGAGAGCTCAATCAGAGGCTGGGGCTGACCCAGAACTATGAGGC 420
QY 421 GTACAGTCACTCTGTGTGTACTTGGTGGCTCAACCGTCAAGGCTGCGGAGTGAAT 480
Db 421 GTACAGTCACTCTGTGTGTACTTGGTGGCTCAACCGTCAAGGCTGCGGAGTGAAT 480
QY 481 CGAGCTAGCTGGCGGCTTGTGTACAGGCTCCAGGCGCTGCGGCGAGCATTCGAGG 540
Db 481 CGAGCTAGCTGGCGGCTTGTGTACAGGCTCCAGGCGCTGCGGCGAGCATTCGAGG 540
QY 541 TGTATGCGGAGCGCTTGGCTTACCCAGCTGCCCCAGGCTCTGCCAGGAGCTGAGCCAGCGCTG 600
Db 541 TGTATGCGGAGCGCTTGGCTTACCCAGCTGCCCCAGGCTCTGCCAGGAGCTGAGCCAGCGCTG 600
QY 601 GGCCCTGCGCTGCGGAGCTTCTCCAGAGATGATGACTTGTGGCTGTGAA 660
Db 601 GGCCCTGCGCTGCGGAGCTTCTCCAGAGATGATGACTTGTGGCTGTGAA 660
QY 661 GGAGCTGAGAGCTGCGCTTACAGCAAGAGCTTCAACCGGCTTAAAGAGAGAT 720
Db 661 GGAGCTGAGAGCTGCGCTTACAGCAAGAGCTTCAACCGGCTTAAAGAGAGAT 720
QY 721 CGAGCTCCAGAGCTTCAAGTCACTCCAGCTTCCAGAGCAATGGTTCTGAGCTTGAC 780
Db 721 CGAGCTCCAGAGCTTCAAGTCACTCCAGCTTCCAGAGCAATGGTTCTGAGCTTGAC 780
QY 781 CCTTAACCCCCACAGCTTCCAGGCGGAGCTGAGCTGTGCTT 819
Db 781 CCTTAACCCCCACAGCTTCCAGGCGGAGCTGAGCTGTGCTT 819

RESULT 4
US-08-792-019B-1
; Sequence 1, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS

STATE: CA
 COUNTRY: USA
 ZIP: 91320
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/792,019B
 FILING DATE: 03-FEB-1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: COOK, ROBERT R.
 REGISTRATION NUMBER: 31,602
 REFERENCE/DOCKET NUMBER: A-442
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 797 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 90..764
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 171..764
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 90..170
 US-08-792-019B-1

Query Match 81.7%; Score 669.4; DB 1; Length 797;
 Best Local Similarity 92.0%; Pred. No. 2.9e-168;
 Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 5 ATTAAGCTTCGCGGAGCGCGCTCGCCCTCCCACTCCGACGCTCTGAGGAGGAG 64
 DB 1 ATTAAGCTTCGCGGAGCGCGCTCGCCCTCCCACTCCGACGCTCTGAGGAGGAG 60
 QY 65 CCG 124
 DB 61 CCGCACCG 119
 QY 125 ATGTTAGCTTGCCTATGACGCTGTGCGACCTCCCTGCGAGTGCAGCTCTTAATCGC 184
 DB 120 ATGTTAGCTTGCCTATGACGCTGTGCGACCTCCCTGCGAGTGCAGCTCTTAATCGC 179
 QY 185 ACAGGAGATCCAGGCGCTGCGCGCTCCATCCAGAAACCTATGACTACCGCGTACCTG 244
 DB 180 ACAGGAGATCCAGGCGCTGCGCGCTCCATCCAGAAACCTATGACTACCGCGTACCTG 239
 QY 245 GAGCATCACTCCGACGCTTAGCTGGAGCTACTGAACTACTCTGGGCGCGCGCTTTCAAC 304
 DB 240 GAGCATCACTCCGACGCTTAGCTGGAGCTACTGAACTACTCTGGGCGCGCGCTTTCAAC 299
 QY 305 GAGCCTGACTTCAATCTCTCGACTGGGCGCGAGAACTCTGCCAGGCGCGCGTCAAC 364
 DB 300 GAGCCTGACTTCAATCTCTCGACTGGGCGCGAGAACTCTGCCAGGCGCGCGTCAAC 359
 QY 365 TTGGAAGTGGCGAGCGCTCATGACGCTGCGGCTGACCGAGAACTATGAGGCGTAC 424
 DB 360 TTGGAAGTGGCGAGCGCTCATGACGCTGCGGCTGACCGAGAACTATGAGGCGTAC 419
 QY 425 AGTCACCTCTGTGTACTTGTGCGTGCCTCAACCGTCAGGCTGCCACAGCTGAATCCGA 484
 DB 420 AGTCACCTCTGTGTACTTGTGCGTGCCTCAACCGTCAGGCTGCCACAGCTGAATCCGA 479
 QY 485 GGTAGCTGCGCGACTTCTGTACCGCTCCAGGCGCTGCGGCGAGCTTCCAGGCTGC 544
 DB 480 GGTAGCTGCGCGACTTCTGTACCGCTCCAGGCGCTGCGGCGAGCTTCCAGGCTGC 539

QY 545 ATGGGAGCGCTTGGCTACCCAGCTGCCCGCGCTCTGCCAGGAGTGCAGCGCTGGCG 604
 DB 540 ATGGGAGCTCTGGGCTACCCAGCTGCCCGCGCTCTGCCAGGAGTGCAGCGCTGGCG 599
 QY 605 CCTGGCGCTGCCCGAGTGCATCTTCTCCAGAAAGATGCATGATCTTGGCTGTGAAGGAG 664
 DB 600 CCTGGCGCTGCCCGAGTGCATCTTCTCCAGAAAGATGCATGATCTTGGCTGTGAAGGAG 659
 QY 665 CTGAGACCTGGCTATGGCGTTTCAGCCAGGAGCTTCAACCGGCTTAAGAGAGATGCAG 724
 DB 660 CTGAGACCTGGCTATGGCGTTTCAGCCAGGAGCTTCAACCGGCTTAAGAGAGATGCAG 719
 QY 725 CCTCCAGCAGCTTCAGTCACTCCCTGCGACTTGGAGGACATGGTTTCTGACCTTCGACCT 783
 DB 720 CCTCCAGCAGCTTCAGTCACTCCCTGCGACTTGGAGGAGCTTGGGCTTCTGACCTTCGACCT 778

RESULT 5

US-08-988-819-1
 ; Sequence 1, Application US/08988819
 ; Patent No. 6054294
 ; GENERAL INFORMATION:

APPLICANT: CHANG, MING-SHI
 TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
 NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
 ADDRESSEE: AMGEN INC.
 STREET: ONE AMGEN CENTER DRIVE
 CITY: THOUSAND OAKS

STATE: CA
 COUNTRY: USA
 ZIP: 91320

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/988,819
 FILING DATE: 12-DEC-1997

CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/792,019
 FILING DATE: 03-FEB-1997

ATTORNEY/AGENT INFORMATION:
 NAME: COOK, ROBERT R.
 REGISTRATION NUMBER: 31,602
 REFERENCE/DOCKET NUMBER: A-442A

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 797 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA

FEATURE:
 NAME/KEY: CDS
 LOCATION: 90..764

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 171..764

FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 90..170

US-08-988-819-1

Query Match 81.7%; Score 669.4; DB 3; Length 797;
 Best Local Similarity 92.0%; Pred. No. 2.9e-168;
 Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 5 ATTAAGCTTCGCGGAGCGCGCTCGCCCTCCCACTCCGCGAGCTCTGAGGAGGAG 64

Db 1 ATTTAAAGCTTGGCGGAGCGCGGCTGCGCCCTCCACCTCCGCCAGCCTCCGGGAGAGGAG 60
QY 65 CGCGCCCG 124
Db 61 CGCGACCG 119
QY 125 ATGTTAGCTTGGCTATGACGGTGTGCGACCTCCCTGAGTGCACAGCTCTTAATCGC 184
Db 120 ATGTTAGCTTGGCTATGACGGTGTGCGACCTCCCTGAGTGCACAGCTCTTAATCGC 179
QY 185 ACAGGAGATCCAGGCG 244
Db 180 ACAGGAGATCCAGGCG 239
QY 245 GAGCATCAACTCCGAGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 304
Db 240 GAGCATCAACTCCGAGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 299
QY 305 GAGCATCAACTCCGAGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 364
Db 300 GAGCATCAACTCCGAGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 299
QY 365 TTGGAGTGTGCGGAGCTTCAATGACAGCTTCAATGACAGCTTCAATGACAGCTTCAATGAC 424
Db 360 TTGGAGTGTGCGGAGCTTCAATGACAGCTTCAATGACAGCTTCAATGACAGCTTCAATGAC 419
QY 425 AGTCACCTCTCTGTGTTACTTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCG 484
Db 420 AGTCACCTCTCTGTGTTACTTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCG 479
QY 485 CGTAGCTTGGCG 544
Db 480 CGTAGCTTGGCG 539
QY 545 ATGGCGACGCTTGGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 604
Db 540 ATGGCGACGCTTGGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 599
QY 605 CCTGCGCTGCG 664
Db 600 CCTGCGCTGCG 659
QY 665 CTGAGAGCTGGCTATGCGGTTGAGCGGCTTCAACCGGCTTCAACCGGCTTCAACCGGCTTCA 724
Db 660 CTGAGAGCTGGCTATGCGGTTGAGCGGCTTCAACCGGCTTCAACCGGCTTCAACCGGCTTCA 719
QY 725 CCTCAGAGCTTCACTACCGCTTCACTACCGCTTCACTACCGCTTCACTACCGCTTCACTACCG 783
Db 720 CCTCAGAGCTTCACTACCGCTTCACTACCGCTTCACTACCGCTTCACTACCGCTTCACTACCG 778

RESULT 6

US-09-016-534-1
; Sequence 1, Application US/09016534
; Patent No. 6143874
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: ELLIOTT, GARY S.
; APPLICANT: SARMIENTO, ULIA
; APPLICANT: SENALDI, GIORGIO
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 90..764
NAME/KEY: mat_peptide
LOCATION: 171..764
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 90..170
US-09-016-534-1

Query Match 81.7%; Score 669.4; DB 3; Length 797;
Best Local Similarity 92.0%; Pred. No. 2.9e-168;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
QY 5 ATTTAAAGCTTGGCGGAGCGCGGCTGCGCCCTCCACCTCCGCCAGCCTCCGGGAGAGGAG 64
Db 1 ATTTAAAGCTTGGCGGAGCGCGGCTGCGCCCTCCACCTCCGCCAGCCTCCGGGAGAGGAG 60
QY 65 CG 124
Db 61 CGCGACCG 119
QY 125 ATGTTAGCTTGGCTATGACGGTGTGCGACCTCCCTGAGTGCACAGCTCTTAATCGC 184
Db 120 ATGTTAGCTTGGCTATGACGGTGTGCGACCTCCCTGAGTGCACAGCTCTTAATCGC 179
QY 185 ACAGGAGATCCAGGCG 244
Db 180 ACAGGAGATCCAGGCG 239
QY 245 GAGCATCAACTCCGAGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 304
Db 240 GAGCATCAACTCCGAGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 299
QY 305 GAGCATCAACTCCGAGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 364
Db 300 GAGCATCAACTCCGAGCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 299
QY 365 TTGGAGTGTGCGGAGCTTCAATGACAGCTTCAATGACAGCTTCAATGACAGCTTCAATGAC 424
Db 360 TTGGAGTGTGCGGAGCTTCAATGACAGCTTCAATGACAGCTTCAATGACAGCTTCAATGAC 419
QY 425 AGTCACCTCTCTGTGTTACTTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCG 484
Db 420 AGTCACCTCTCTGTGTTACTTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCG 479
QY 485 CGTAGCTTGGCG 544
Db 480 CGTAGCTTGGCG 539
QY 545 ATGGCGACGCTTGGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 604
Db 540 ATGGCGACGCTTGGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 599


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; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5087 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 137..138
; OTHER INFORMATION: /product= "INTERVENING UNSEQUENCED
; OTHER INFORMATION: REGION OF >1KB"
US-08-792-019B-3

Query Match          52.5%; Score 429.6; DB 1; Length 5087;
Best Local Similarity 90.4%; Pred. No. 2e-104;
Matches 459; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 276 ACCTGAACACTACCTGGGCCCCCTTTCAACGAGCCTGACTTCAATCCCTCCGACTGGGG 335
Db 3363 AGCTGAACACTACCTGGGCCCCCTTTCAACGAGCCTGACTTCAATCCCTCCGACTGGGG 3422

Qy 336 CAGAAACTCTGCCAGGGCCAGCTCACTTGGAGTGTGGCGAGCCTCAATGACAGGC 395
Db 3423 CAGAGACTCTGCCAGGGCCAGCTTGTGACTTGGAGGTGTGGCGAGCCTCAATGACAAAC 3482

Qy 396 TGGCGCTGACCCAGAACTATGAGCGGTACAGTCACTCTCTGTGTTACTTGGTGGGCTCA 455
Db 3483 TGGCGCTGACCCAGAACTATGAGCGGTACAGTCACTCTCTGTGTTACTTGGTGGGCTCA 3542

Qy 456 ACCGTGAGGTGCGACAGCTGAACTCCGACGTGAGCCTGGCTATGGCGTTGACGCAAG 695
Db 3543 ACCGTGAGGTGCGACAGCTGAACTCCGACGTGAGCCTGGCTATGGCGTTGACGCAAG 3782

Qy 696 ACTTCAACCGGCTTAAGAAGATGACGCTCCAGCAGCTTCCAGTCAACCTCGACTTGG 755
Db 3783 ACTTCAACCGGCTTAAGAAGATGACGCTCCAGCAGCTTCCAGTCAACCTCGACTTGG 3842

Qy 756 AGGCACATGTTTCTGACCTTGTGACCTT 783
Db 3843 GGGCTCATGGCTTCTGACTTGTGACCTT 3870

RESULT 9
US-08-988-819-3
; Sequence 3, Application US/08988819
; Patent No. 6054294
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS

```

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; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5087 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 137..138
; OTHER INFORMATION: /product= "INTERVENING UNSEQUENCED
; OTHER INFORMATION: REGION OF >1KB"
US-08-988-819-3

Query Match          52.5%; Score 429.6; DB 3; Length 5087;
Best Local Similarity 90.4%; Pred. No. 2e-104;
Matches 459; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 276 ACCTGAACACTACCTGGGCCCCCTTTCAACGAGCCTGACTTCAATCCCTCCGACTGGGG 335
Db 3363 AGCTGAACACTACCTGGGCCCCCTTTCAACGAGCCTGACTTCAATCCCTCCGACTGGGG 3422

Qy 336 CAGAAACTCTGCCAGGGCCAGCTCACTTGGAGTGTGGCGAGCCTCAATGACAGGC 395
Db 3423 CAGAGACTCTGCCAGGGCCAGCTTGTGACTTGGAGGTGTGGCGAGCCTCAATGACAAAC 3482

Qy 396 TGGCGCTGACCCAGAACTATGAGCGGTACAGTCACTCTCTGTGTTACTTGGTGGGCTCA 455
Db 3483 TGGCGCTGACCCAGAACTATGAGCGGTACAGTCACTCTCTGTGTTACTTGGTGGGCTCA 3542

Qy 456 ACCGTGAGGTGCGACAGCTGAACTCCGACGTGAGCCTGGCTATGGCGTTGACGCAAG 515
Db 3543 ACCGTGAGGTGCGACAGCTGAACTCCGACGTGAGCCTGGCTATGGCGTTGACGCAAG 3602

Qy 516 AGGGCTGTGGGAGCATTCAGTGTGAGGAGCTGAGCCTGGCTATGGCGTTGACGCAAG 575
Db 3603 AGGGCTGTGGGAGCATTCAGTGTGAGGAGCTGAGCCTGGCTATGGCGTTGACGCAAG 3662

Qy 576 CTCTGCCAGGACTGAGCCAGCCTGGGCCCCCTGGGCCCCCTGGCCACAGTGAATTCCTCCAGA 635
Db 3663 CGCTGCCTGGGACTGAAACCCACTTGGACTCTCTGGCCCCCTGGCCACAGTGAATTCCTCCAGA 3722

Qy 636 AGATGATGACTTCTGGCTGTGAGGAGCTGAGCCTGGCTATGGCGTTGACGCAAG 695
Db 3723 AGATGATGACTTCTGGCTGTGAGGAGCTGAGCCTGGCTATGGCGTTGACGCAAG 3782

Qy 696 ACTTCAACCGGCTTAAGAAGATGACGCTCCAGCAGCTTCCAGTCAACCTCGACTTGG 755
Db 3783 ACTTCAACCGGCTTAAGAAGATGACGCTCCAGCAGCTTCCAGTCAACCTCGACTTGG 3842

Qy 756 AGGCACATGTTTCTGACCTTGTGACCTT 783
Db 3843 GGGCTCATGGCTTCTGACTTGTGACCTT 3870

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RESULT 10
 US-09-016-534-3
 ; Sequence 3, Application US/09016534
 ; Patent No. 6143874
 ; GENERAL INFORMATION:
 ; APPLICANT: CHANG, MING-SHI
 ; APPLICANT: ELLIOTT, GARY S.
 ; APPLICANT: SARMIENTO, ULLA
 ; APPLICANT: SENALDI, GIORGIO
 ; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: AMGEN INC.
 ; STREET: ONE AMGEN CENTER
 ; CITY: THOUSAND OAKS
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 91320
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,534
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/792,019
 ; FILING DATE: 03-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: COOK, ROBERT R.
 ; REGISTRATION NUMBER: 31,602
 ; REFERENCE/DOCKET NUMBER: A-442B
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5087 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 137..138
 ; OTHER INFORMATION: /product= "INTERVENING UNSEQUENCED
 ; OTHER INFORMATION: REGION OF >1KB"
 ; US-09-016-534-3

Query Match 52.5%; Score 429,6; DB 3; Length 5087;
 Best Local Similarity 90.4%; Pred. No. 28-104; Indels 0; Gaps 0;
 Matches 459; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
 QY 276 ACCTGAACCTACCTGGGGCCCTTTCAACAGAGCTGACTTCAATCTCTGACTGGGGG 335
 DB 3363 AGCTGAACCTACCTGGGGCCCTTTCAACAGAGCTGACTTCAATCTCTGACTGGGGG 3422
 QY 336 CAGAACTCTGCCAGGCGCAGCTCACTTGAAGTGTGGGAGAGCTCAATGACAGGC 395
 DB 3423 CAGAGACTCTGCCAGGCGCAGCTTGTGACTTGGAGTGTGGGAGAGCTCAATGACAAAC 3482
 QY 396 TGGGGCTGACCCAGAACTATGAGGCGTACAGTCACCTCTCTGTGTACTTGGCTGCCCTCA 455
 DB 3483 TGGGGCTGACCCAGAACTATGAGGCGTACAGTCACCTCTCTGTGTACTTGGCTGCCCTCA 3542
 QY 456 ACCGTAGAGTGCACAGCTGAACCTCGAGTACCTGCGCCACTTCTGTACAGCCTCC 515
 DB 3543 ACCGTAGAGTGCACAGCTGAACCTCGAGTACCTGCGCCACTTCTGTACAGCCTCC 3602
 QY 516 AGGGCTGTGGGCGAGCATTTGCGGCGTCTATGCGGAGCGCTTGGCTACCCACTGCCCCAGC 575
 DB 3603 AGGGCTGTGGGCGAGCATTTGCGGCGTCTATGCGGAGCGCTTGGCTACCCACTGCCCCAGC 3662

QY 576 CTCTGCCAGGAGCTGAGCCAGCCTGGGCCCCCTGGGCCCCCTGCCACAGTGACTTCTCTCCAGA 635
 DB 3663 CGCTGCTGGGAGCTGAACCCACTTGGACTCTTGGGCCCCCTGCCACAGTGACTTCTCTCCAGA 3722
 QY 636 AGATGATGACTTCTGGCTGCTGAAGGAGCTGCAGACCTGGGCTATGGGCTTCAGCCAAAG 695
 DB 3723 AGATGAGCAGCTTCTGGCTGCTGAAGGAGCTGCAGACCTGGGCTATGGGCTTCAGCCAAAG 3782
 QY 696 ACTTCAACCGGCTTAAGAAGAAGATGCAGCCTCCAGCAGCTTCAGTCACCTTGCACCTTGG 755
 DB 3783 ACTTCAACCGGCTCAAGAAGAAGATGCAGCCTCCAGCAGCTTCAGTCACCTTGCACCTTGG 3842
 QY 756 AGCAGATGTTTCTGACCTCTGACCTT 783
 DB 3843 GGGCTCATGGCTTCTGACTTCTGACCTT 3870

RESULT 11
 US-09-106-182-7
 ; Sequence 7, Application US/09106182
 ; Patent No. 6046035
 ; GENERAL INFORMATION:
 ; APPLICANT: Shi, Yanguu
 ; APPLICANT: Ruben, Steve
 ; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc
 ; STREET: 9410 Key West Ave
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/106,182
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/051,053
 ; FILING DATE: 30-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brookes, A. Anders
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF385
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8504
 ; TELEFAX: 301-309-8439
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 396 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-09-106-182-7

Query Match 6.3%; Score 52; DB 3; Length 396;
 Best Local Similarity 85.3%; Pred. No. 0.00011;
 Matches 58; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 716 AAGATGAGCAGCTTCAGCAGCTTCAGTCACCTGCACTTGGAGGCACATGTTTCTGACCT 775
 DB 4 ACGAGGAGAGCTCCAGCAGCTGACAGCTGACCTGACCTGGGGGCTCATGGCTTCTAACTT 63
 QY 776 CTGACCTT 783
 DB 64 CTGACCTT 71

APPLICANT: Seedorf, Klaus
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
OF TKA-1 RELATED
DISORDERS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,037

FILING DATE: June 13, 1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/005,167

FILING DATE: October 13, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 220/156

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1642 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 97...1446

US-08-665-037-1

Query Match 5.2%; Score 42.4; DB 2; Length 1642;
Best Local Similarity 52.9%; Pred. No. 0.061;
Matches 91; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 512 CTCAGGGCTGCTGGGCGAGCTGTCAGGTGTCATGGGAGCGCTTGGCTACCCACTGCC 571

Db 379 CTCGGCGGGCGAGCTGACCTGTACCGAGGAGATGGCCGAGGAGGCTCCACCCGCC 438

QY 572 CAGCCTCTCCAGGAGTACGAGCGCTGGGCCCTGGCCCTGCCACAGTGACTTCCTC 631

Db 439 CAGACCCCTGGAGCGGAGCGAGCTGGGCACACACCGGAGGAGCTCCGAGCT 498

QY 632 CAGAAGATGATGACTTCTGGCTGTGAAGGAGCTGCAGACCTGGCTATGCC 683

Db 499 GGCAAGAAGATGTCAGTGGGCCCTGAGGGAGCTGGCCCTCGGCTCTGCC 550

RESULT 15
US-08-666-067-1
Sequence 1, Application US/08666067
Patent No. 5922842
GENERAL INFORMATION:
APPLICANT: Seedorf, Klaus
APPLICANT: Ulrich, Axel
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
OF TKA-1 RELATED
DISORDERS

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,067
FILING DATE: June 13, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,421
FILING DATE: October 13, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 220/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1642 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 97...1446
US-08-666-067-1

Query Match 5.2%; Score 42.4; DB 2; Length 1642;
Best Local Similarity 52.9%; Pred. No. 0.061;
Matches 91; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 512 CTCAGGGCTGCTGGGCGAGCTGTCAGGTGTCATGGGAGCGCTTGGCTACCCACTGCC 571

Db 379 CTCGGCGGGCGAGCTGACCTGTACCGAGGAGATGGCCGAGGAGGCTCCACCCGCC 438

QY 572 CAGCCTCTCCAGGAGTACGAGCGCTGGGCCCTGGCCCTGCCACAGTGACTTCCTC 631

Db 439 CAGACCCCTGGAGCGGAGCGAGCTGGGCACACACCGGAGGAGCTCCGAGCT 498

QY 632 CAGAAGATGATGACTTCTGGCTGTGAAGGAGCTGCAGACCTGGCTATGCC 683

Db 499 GGCAAGAAGATGTCAGTGGGCCCTGAGGGAGCTGGCCCTCGGCTCTGCC 550

Search completed: August 16, 2004, 09:35:25
Job time : 68.3589 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 06:43:28 ; Search time 13.5 Seconds
(without alignments)
1603.192 Million cell updates/sec

Title: US-09-931-704-5

Perfect score: 1224

Sequence: 1 MDLRAGDSWGMGLCTVLM.....KKQMPPAAVTLLEAHGF 225

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118.5	9.7	203	JC4645	cardiotrophin-1 -
2	110.5	9.0	203	I49153	cardiotrophin-1 -
3	93.5	7.6	640	T34916	transferase - Stre
4	92.5	7.6	200	AD3633	hypothetical prote
5	92	7.5	332	C86182	hypothetical prote
6	91.5	7.5	201	G02312	cardiotrophin-1 -
7	90	7.4	195	JH0680	ciliary neurotroph
8	90	7.4	733	F82965	hypothetical prote
9	89	7.3	733	D83588	conserved hypotet
10	86	7.0	1313	T38943	probable guanine n
11	85.5	7.0	389	F72511	probable cystathio
12	85.5	7.0	560	C38604	poly(3-hydroxyalka
13	85	6.9	520	B75332	extracellular solu
14	84	6.9	741	A83271	hypothetical prote
15	83	6.8	272	T35231	hypothetical prote
16	83	6.8	955	T00247	zinc finger protei
17	83	6.8	1561	T00248	zinc finger protei
18	80.5	6.6	1006	T42782	probable alpha-man
19	80	6.5	382	A82196	two-component hybr
20	80	6.5	1179	T04594	TNW resistance pro
21	79.5	6.5	294	T32947	hupK protein - Rho
22	79.5	6.5	316	T34553	hypothetical prote
23	79.5	6.5	512	S21171	activin receptor S
24	79.5	6.5	542	A82965	hypothetical prote
25	79.5	6.5	644	JC5119	anti-mullerian hor
26	79	6.5	1132	A35038	MHC class III hist
27	78.5	6.4	338	T45394	hypothetical prote
28	78.5	6.4	400	AF0873	probable monooxyge
29	78.5	6.4	522	D87123	conserved hypotet

30 78.5 6.4 531 2 B83422 probable serine/th
31 78.5 6.4 571 2 H70623 probable potassium
32 78.5 6.4 1844 2 S01956 hypothetical prote
33 78 6.4 232 2 AG3157 hypothetical prote
34 78 6.4 378 2 D83381 hypothetical prote
35 78 6.4 427 1 RRYC65 RNA-directed DNA p
36 78 6.4 515 2 T37982 RNA-directed prote
37 78 6.4 917 2 S40178 RNA-directed prote
38 78 6.4 917 2 D89891 RNA-directed prote
39 77.5 6.3 572 2 B72714 RNA-directed prote
40 77.5 6.3 1182 2 I48378 RNA-directed prote
41 77 6.3 322 2 T23891 RNA-directed prote
42 77 6.3 327 2 AF2887 RNA-directed prote
43 77 6.3 327 2 C97663 RNA-directed prote
44 77 6.3 411 2 F75439 RNA-directed prote
45 77 6.3 1031 2 F83561 RNA-directed prote

ALIGNMENTS

RESULT 1

JC4645

cardiotrophin-1 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000

C/Accession: JC4645

R;Ishikawa, M.; Saito, Y.; Miyamoto, Y.; Kuwahara, K.; Ogawa, E.; Nakagawa, O.; Harada, T.

Biochem. Biophys. Res. Commun. 219, 377-381, 1996

A;Title: cDNA cloning of rat cardiotrophin-1 (CT-1): Augmented expression of CT-1 gene in

A;Reference number: JC4645; MUID:96193659; PMID:8604995

A;Accession: JC4645

A;Molecule type: mRNA

A;Residues: 1-203 <ISH>

A;Cross-references: DDBJ:D78591; NID:gi256926; PIDN:BAAL1427.1; PID:gi256927

C;Genetics:

A;Gene: CT-1

C;Keywords: cardiac muscle; cytokine; heart

Query Match 9.7%; Score 118.5; DB 2; Length 203;
Best Local Similarity 27.5%; Pred. No. 0.0015;
Matches 49; Conservative 26; Mismatches 84; Indels 19; Gaps 6;

QY 40 IOKTVDLTRYLSEHQRLAGTYLNYLGPFPNPPNPPRL---GAETLPRAVTVNLEWRES 96
DB 27 IRQTNELARLLTKYADQLLEEVYQQGGPFGLPGSPPLPLAGLSGAPSPHAGLPV--- 83
QY 97 LNDRLRLTONYEAYSHLLCYLRGLNRQAA-----TAELRRSLAHFCTSLQGLLSIAGVM 151
DB 84 -SERLR--QDAALSAIPALLDAVRRQAEINPRAPRLRLSRLEDAARQVRLGAATVTL 140
QY 152 ATLGV----PLPQPLPGTEPAWPGPAHSDFLOKMDDFWLLKELQTLWRSKADFNRL 205
DB 141 AALGAARQGVPEPV-ATSLFTSNAGVFSKVLGLHVCGLYGEWVSRTEGDLGQL 197

RESULT 2

I49153

cardiotrophin-1 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C/Accession: I49153

R;Pennica, D.; King, K.L.; Shaw, K.J.; Luis, E.; Rullanas, J.; Luch, S.; Darbonne, W.C.;

Proc. Natl. Acad. Sci. U.S.A. 92, 1142-1146, 1995

A;Title: Expression cloning of cardiotrophin 1, a cytokine that induces cardiac myocyte

A;Reference number: I49153; MUID:95166785; PMID:7862649

A;Accession: I49153

A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-203 <RES>

A;Cross-references: EMBL:U18366; NID:g710331; PIDN:AAC52173.1; PID:g710332

C;Genetics:

A;Gene: ctfl

C;Keywords: cytokine; glycoprotein
F;164/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.0%; Score 110.5; DB 2; Length 203;
Best Local Similarity 27.4%; Pred. No. 0.0084;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

QY 40 IOKTVDLRYLEHQLRSLAGTVNLVGPFPNEPDPNPRLL---GAETLPRAVTVNLVWRS 96
DB 27 IQKTNLAELLTKYAEQLLEEVQOQGFGLPGFSPRLPLAGLSGAPSHAGLPV--- 83
QY 97 LNDRLRLTONYEAYSHLLCYLRLGNRQA---TAELRRSLAHFCTSLQGLLGSIAQVM 151
DB 84 -SERLR--QDAALSVPALLDAVRRQALNPRAPIRLRLSRLEDAARQVRAALGAAVETVL 140
QY 152 ATLGVPPLPQPLGTTPA-----WAPGPAHSDFLQKMDDFWLLKELQTLWRSKDFNRL 205
DB 141 AALGAAARG--PGPEPVTATLFTANSTAGIFSAPKVLGHVCGLYGEWVSRTEGDLGQL 197

RESULT 3
T34916
transferase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 02-Sep-2000
C;Accession: T34916
R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z21558
A;Accession: T34916
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-640 <OLI>
A;Cross-references: EMBL:AL021409; PIDN:CAA16181.1; GSPDB:GN000070; SCODEB:SC3F7.10
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCODEB:SC3F7.10
C;Superfamily: Glycine C-acetyltransferase homology
F;287-624/Domain: glycine C-acetyltransferase homology <GCA>

Query Match 7.6%; Score 93.5; DB 2; Length 640;
Best Local Similarity 28.3%; Pred. No. 1.3;
Matches 52; Conservative 12; Mismatches 63; Indels 57; Gaps 9;

QY 22 LPAPVAPALNTGDPGPGPSIQKTYDLYRYLEHQL---RSLAGTVNLVGLPFPNEPDPNPR 78
DB 100 LPAPVPA-EGTGDPTVSAVVAAMRQYQYRQHQGLDADLEG-----E 140
QY 79 LGAEETLPRAVTVNLVWRSNDRLRLTONYEAYSHLLCYLRLGNRQAATAELRRSLAHFCT 138
DB 141 LGVDSVVLSVVAEA---TERLGLT-----GAAPDAAGATTLRALA---D 179
QY 139 SLOGLLGSAGVWATLGYLPQLPCTEPAPWAPGPAHSDFLQKMDDFWLLKELQTLWRS 198
DB 180 ALRGL-----VAAAPGTAVPEAAPATGAA-APAPGRSGNAP-----APGADGWDHRS 225
QY 199 AKDF 202
DB 226 MKDF 229

RESULT 4
AD3633
hypothetical protein BMEII0989 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AD3633
R;DeiVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Leticia
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AD3633

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-200 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL54231.1; PID:G17985203; GSPDB:GN00191
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0989
A;Map position: II

Query Match 7.6%; Score 92.5; DB 2; Length 200;
Best Local Similarity 23.9%; Pred. No. 0.38;
Matches 55; Conservative 21; Mismatches 89; Indels 65; Gaps 11;

QY 10 GMUACICTLVHLPAVPALNRGDPGPGPSIQKTYDLYRYLEHQLRSLAGTVNLVGLPFP 69
DB 2 GLLAGAALV---LPSLPAAKATQQAAMPNPATSPHOADVIL---LRGFADISTGTI--- 51
QY 70 NEPDFNPRLGAEETLPRAVTVNLVWRSNDRLRLTONYEAYSHLLCYLRLGNRQA 124
DB 52 -----DEIGAE-LQAAGVNAHVQGHAAARLVNLNIVADQCKNGHLPVVLIGHSLGANA 103
QY 125 A---TAELRRSLAHFCTSLQGLLGSAGVWATLGYLPQLPCTEP---PPAW--- 169
DB 104 AIYIAEELERR-----GIAVDYMATFAATGPDPLFCNVRVNVNFYFKHGWGL 151
QY 170 --APGPAHSDFLQKMDDFWLLKELQTLWRSKDFNRLK-KMQPPAAASV 216
DB 152 PLVPGPRFHGHLENRD-----PSNAKDVGHFNIKQRPLOAEV 189

RESULT 5
G86182
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G86182
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86182
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-332 <STO>
A;Cross-references: GB:AE005172; NID:g7211973; PIDN:AAF40444.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 7.5%; Score 92; DB 2; Length 332;
Best Local Similarity 25.9%; Pred. No. 0.79; 73; Indels 66; Gaps 12;
Matches 57; Conservative 24; Mismatches 89

QY 23 PAVPALNRGDPGPGPSIQKTYDLYRYLEHQLRSLAGTVNLVWRSNDRLRLTONYEAYSHLLCYLRLGNRQA 124
DB 113 PSVTAGNLGVP-PPPSF--TYDPGPEYQRMESLQOQFIRERNPPQIRPLRGLGSPVG 169
QY 65 LGPPFNPDPNPRPLGAEETLPRAVTVNLVWRSNDRLRLTONYEAYSHLLCYLRLGNRQA 124
DB 170 LGPTRASQFLQPRVA---PPPTSILDTSRNRKASK-----DGLAVVRG--RKV 215
QY 125 ATAEELRSL-----AHFCTSLQGLLGSAGVWATLGYLPQLPCTEP---GTEPAWA 170
DB 216 RITEGSSSLYSLSGSLKNGAHV-----GIQPSRSGIMK---PLPKPLPDLVLTTSVP 266
QY 171 PGPAHSDFLQKMDDFWLLKELQTLWRSKDFNRLKMQ 210

Db 267 DDPDESADEKDEEAVQVL-----SEKDL--LKRHIE 298

RESULT 6
G02312
cardiotrophin-1 - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C/Accession: G02312
R/Wood, W.I.
submitted to the EMBL Data Library, December 1995
A/Reference number: H01035
A/Accession: G02312
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-201 <WOO>
A/Cross-references: EMBL:U43030; NID:g1151149; PID:g1151150
C/Genetics:
A/Gene: GDB:CTP1; CT-1
A/Cross-references: GDB:567078
A/Map position: lp22-lp22

Query Match 7.5%; Score 91.5; DB 2; Length 201;
Best Local Similarity 25.7%; Pred. No. 0.47;
Matches 45; Conservative 23; Mismatches 92; Indels 15; Gaps 5;

QY 40 IOKTYDITRYLEHQLRSLAGTYLNLGPPNEPDPNPRILGASTLPRTATVNLVWRSND 99
Db 27 IRQTHSAHLTKVAEQLLQEVOLQDGFSPRLPVAGL-SAPAPSHAGLPVHE 85
QY 100 RLRLTONYEAYSHLLCYLRGLNRQA-----TAELRSLAHFCTSLQGLGSLAGVWATL 154
Db 86 RLRL--DAALALPPLLDVACRQAEINPRAPRLRLLEDAARQARALGAEEALLAAL 143
QY 155 QY-----PLPQPLPGTEPAWAPGAHSDFLQKMDDFWLKELQTLWRSKDFNRL 205
Db 144 GAANRGPRAEPPAATASA---ASATGVFPKVLGLRCVGLREWLSRTEGDLQL 195

RESULT 7
JH0680
ciliary neurotrophic factor - chicken
N/Alternate names: growth-promoting activity protein
C/Species: Gallus gallus (chicken)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
C/Accession: JH0680; PQ0057
R/Leung, D.W.; Parent, A.S.; Cachianes, G.; Esch, F.; Coulombe, J.N.; Nikolics, K.; Ecker
Neuron 8, 1045-1053, 1992
A/Title: Cloning, expression during development, and evidence for release of a trophic f
A/Reference number: JH0680; MUID:92304573; PMID:1610564
A/Accession: JH0680
A/Molecule type: mRNA
A/Residues: 1-195 <LEU>
A/Cross-references: GB:M80827; NID:g211822; PID:AAA48784.1; PID:g211823
A/Experimental source: eye
R/Eckenstein, F.P.; Esch, F.; Holbert, T.; Blacher, R.W.; Nishi, R.
Neuron 4, 623-631, 1990
A/Title: Purification and characterization of a trophic factor for embryonic peripheral
A/Reference number: PQ0057; MUID:90211978; PMID:2322465
A/Accession: PQ0057
A/Molecule type: protein
A/Residues: 155-166, X, 168-175 <ECK>
A/Experimental source: sciatic nerves
C/Comment: This is a neurotrophic protein.
C/Superfamily: ciliary neurotrophic factor
C/Keywords: growth factor

Query Match 7.4%; Score 90; DB 2; Length 195;
Best Local Similarity 27.7%; Pred. No. 0.63;
Matches 52; Conservative 21; Mismatches 83; Indels 32; Gaps 10;

QY 46 LTRYLEHQLRSLAGTYLNLGPPNEPDPNPRILGASTLPRTATVNLVWRSNDRLRLTQ 105

Db 23 LARKMRSDVTDLLDIYVERQG-----LDASISVAADVGVPTAAV--ERWAEQTGTORLLD 75

QY 106 N---YEAYSHLLCYLRGLNRQA---ATAELRSLA-----HFCTSLQGLGSLAGVWA 152
Db 76 NLAAVRAFRFTLLAQMLEEQRELLGDTDAELGAPALAMLLQVSAFVYHLELL-----ELE 130
QY 153 TLGYPLPQPLPGTEPAWAPGAHSDFLQKMDDFWLKELQTLWRSKDFNRLKKMQPP 212
Db 131 SRGAPAE--GSEPP-AP-PRLSLFEQKLRGLRVRELAQWAVRSVRDLRLQLSK--HGP 183
QY 213 AASVTIHL 220
Db 184 GSGAALGL 191

RESULT 8
F82965
hypothetical protein PA5441 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C/Accession: F82965
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A/Reference number: AB2950; MUID:20437337; PMID:10984043
A/Accession: F82965
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-733 <STO>
A/Cross-references: GB:AE004957; GB:AE004091; NID:g9951770; PIDN:AAG08826.1; GSPDB:GN001
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA5441

Query Match 7.4%; Score 90; DB 2; Length 733;
Best Local Similarity 23.9%; Pred. No. 3.2;
Matches 48; Conservative 24; Mismatches 81; Indels 48; Gaps 8;

QY 23 PAVPALNRTGDPGPGPS:QKTYDITRYLEHQLRSLAGTYLNLGPPNEPDPNPRILGAE 82
Db 102 PALPAASEAETPPAPAPAPLAELAR-----QMGAE 132
QY 83 TLPRTATVNLVWRSNDRLRLTONYEAYSHLLCYLRGLNRQAATAELR-RSLAHFCTSLQ 141
Db 133 ALPEKIAGAEFFEGSGCRSNDQDSA---LAFLRQV-RDAGLGEAETKALAN---SRL 184
QY 142 GLLGSIAGVMTATGYPLPQPLPGTEPAWAPGAHSDFLQKMDDFWLKELQTLWRSKAD 201
Db 185 DLGACGWEQELGGLVLAQ---GVES--AAGKAPATYLEAAANFYSGR-----PDEAEQG 234
QY 202 FNRLKKKQVPPAASVTIHL 222
Db 235 FRALQDVSPWLKETALYLQA 255

RESULT 9
D83588
conserved hypothetical protein PA0454 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C/Accession: D83588
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: AB2950; MUID:20437337; PMID:10984043
A/Accession: D83588
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-733 <STO>

A;Cross-references: GB:AE004483; GB:AE004091; NID:9946313; PIDN:AA03843.1; GSPDB:GN001

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA0454

C;Superfamily: hypothetical protein H11680

Query Match 7.3%; Score 89; DB 2; Length 733;

Best Local Similarity 25.8%; Pred. No. 4;

Matches 57; Conservative 26; Mismatches 64; Indels 74; Gaps 13;

28 LNRTGDPGGPSIQKTYLTYLE-----HQLRSAGTYLVNLPPEPDP--FNPP 77

230 LNRLGHGRPGPKV-----SRLLKYFTIAQDVHERASSSHYPYVRLAEAFHSDVLRFCQ 283

78 RL-----GAETLPRTATNVWRSINLDRILTONYEAYSHLLCYLRGLNQAATABLERR 131

264 RLNNQGGKACQALARA-----INLRQFPD-YA-----DRELALEDLQA 320

132 SLAHF-----CTSLOGL-----LGSIAGMATIGYPLPQPLGTEPAWAGPAHSDFLQXMD 184

321 SLEHLRQOSNPAMKGLRSLGALANLTLDKLT-----AGASNPDAIDEDQ 368

185 FWLLKELQTLWRSKAD-FNRLKKKQMPAASVTLHLEAHG 224

369 SALLDRSP-----RSKDAFERLRQQLTP-----TSLLFRHG 400

RESULT 10

T38943

probable guanine nucleotide binding protein - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T38943

R;Skellton, J.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, May 1997

A;Reference number: Z21819

A;Accession: T38943

A;Status: preliminary;

A;Molecule type: DNA

A;Residues: 1-1313 <SK>

A;Cross-references: EMBL:Z95396; PIDN:CA08769.1; GSPDB:GN00066; SPDB:SPAC57A7.11

A;Experimental source: strain 972h; cosmid c57A7

C;Genetics:

A;Gene: SPDB:SPAC57A7.11

A;Map position: 1

Query Match 7.0%; Score 86; DB 2; Length 1313;

Best Local Similarity 22.2%; Pred. No. 16;

Matches 58; Conservative 31; Mismatches 84; Indels 88; Gaps 12;

15 LCTVLMHLEAV--PALNR-----TGDPGPGFSI-----QKTYDLYLTYLEHQLRS 56

811 LAFLLQLHLPALHKAISKDITNSVTSPKPHFPVPSVSENKILNRSFSLRSLKGLALS 870

57 LAG-----TYLVNLT-----GPP-FNEPDPNPRCAETLPRTATNV 91

871 LAGSDRASELLSINGENKPAESNLNHLTSKAVPGPPAFNELEYQ-----SELDPLTYSYLF 926

92 EYVRSINLRLITONYEAYSHLLCYLRGL-----NQQAATAELRLSLAHFCTS-----LQ 142

927 DMSRKYFTPEQRPNEDEFGSICYNQLWRNRENEKLIYRPLAEYSTNGRWNQMLMT 986

143 LGSIAGMATIGYPLPQPLGTEPAWAGPAHSDFLQXMDFFWLKE-----LOTWLWRS 199

987 FNNITIA-----PRKLMFHQFEDQLITLGDKDIIVQVWDWRN 1022

200 KDFNRLKKKQMPAASVTLHL 220

1023 RLNSFK-----TSASATINV 1038

RESULT*11

F72511

probable cystathionine gamma-synthase APE2068 - Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C;Accession: F72511

R;Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ku

DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyru

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: F72511

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-389 <KAW>

A;Cross-references: DDBJ:AP000063; NID:G5105654; PIDN:BAA81078.1; PID:G5105766

A;Experimental source: strain K1

C;Genetics:

A;Gene: APE2068

C;Superfamily: O-succinylhomoserine (thiol)-lyase

Query Match 7.0%; Score 85.5; DB 2; Length 389;

Best Local Similarity 22.9%; Pred. No. 3.8;

Matches 47; Conservative 20; Mismatches 77; Indels 61; Gaps 8;

43 TYDLTRYLHQRLSLAGTYLVNLYGPPPEPDPNPRGLGAETLPRTATNVLEWRSL----- 97

107 TYGSTRSLLEMLSSITGIEVRLAGPPWED-----LLDLVCWADLIIVES 150

98 --NDRRLITONYEAYSHLLCYLRGLNROQAATAELR-----RSL---AHFCTS 139

151 MANPTURVPP-----LSGIYREAGSGVRVVDVNTATPIAYEPLERGAY--S 197

140 LQGLLSIAGVWATIGYPLPQPL-PTETPAWAGPAHSDFLQXMDFFWLKELQTLWRS 198

198 LESLTKVIAGHDVVGSLSGRVEEDLEPLWNKRKILGTIMQPIDAY-----LAWRG 249

199 AKDFNRLKKKQMPAASVTLHLEAH 223

250 MKTLKARFEAQSRAAVEVAEWLESH 274

RESULT 12

C38604

poly(3-hydroxyalkanoate) polymerase (EC 2.7.7.-) 3 - Pseudomonas oleovorans

C;Species: Pseudomonas oleovorans

C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 08-Sep-2000

C;Accession: C38604

R;Huisman, G.W.; Wink, E.; Meima, R.; Kazemier, B.; Terpstra, P.; Witholt, B.

J. Biol. Chem. 266, 2191-2198, 1991

A;Title: Metabolism of poly(3-hydroxyalkanoates) (PHAs) by Pseudomonas oleovorans. Ident

A;Reference number: A38604; MUID:91115830; PMID:1989978

A;Accession: C38604

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-560 <HUI>

A;Cross-references: GB:M58445; NID:G151441; PIDN:AAA25934.1; PID:G151444

C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbc

C;Keywords: nucleotidyltransferase

Query Match 7.0%; Score 85.5; DB 2; Length 560;

Best Local Similarity 30.2%; Pred. No. 6;

Matches 38; Conservative 16; Mismatches 43; Indels 29; Gaps 7;

77 PRIGAETLPRTATNVLEWRSINLDRILRLITONYEAYSHLLCYLRGLNROQAATAELRSL--A 134

5 PAKGTPLPATSNVQ-----NAILGLRGR-----DLISLRLNVSRQS-----LRHPLHTA 50

135 HFCTSLQGLLSIAGVWATIGYPLPQPLG-----TPPAWAGPAHSDFLQXMDFFWLKE 190

51 HHLALGGQLGRV-----ILGDTPLQFNPRDRPFSPTWSQNFYRRLQA-----YLAWQ 101

191 LOTWLW 196

102 KQRLW 107

Db 478 LL-----LPALLPSSPPVWVG-----RAEVRVLDVGQGLAVLVRTRE-----HVLLYDSG 522
QY 120 LNRQAA-----TAE LRSLAHFCTSLQGLGSIAGVMATLGYPL-----PQ 160
Db 523 A-RQAFDGMGRVVPVLRSLDRLR-----LQGLLLSHADNDHAGAPTVAERFPVPV 573
QY 161 PLFPTGTEPAWAPGASHDFLQKMDDFWLKELQTLWRSKADFNRLKKMKQPPAASVTLHL 220
Db 574 WLVSQEPARLPSPFLPADSCDRSWSWDGVVFPQWAAQAQDSN-----DRSCVLRV 624
QY 221 EAHG 224
Db 625 EADG 628

RESULT 15
T35231
hypothetical protein SC5C7.24c SC5C7.24c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T35231
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21572
A:Accession: T35231
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-272 <SEE>
A:Cross-references: EMBL:AL031515; PIDN:CRA20636.1; GSPDB:GN00070; SCODEB:SC5C7.24c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCODEB:SC5C7.24c

Query Match 6.8%; Score 83; DB 2; Length 272;
Best Local Similarity 23.9%; Pred. No. 4.2;
Matches 38; Conservative 15; Mismatches 50; Indels 56; Gaps 7;
QY 23 PAVPALN-----RTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTVLYLGGPEN-----70
Db 95 PAIGALREGVERLIRGYEPYALVDATYRVLAANGIAMLDGVAEHLITPLNAIRLT 154
QY 71 -EPDFNPPLGAEITLPRATVNLVWRSNLDRRLRLTQNYEAYSHLLCYLRLNQRAATAEL 129
Db 155 LHPDGLAPRIR-----NLREWR-----GHLL-----EQM 178
QY 130 RRSLLA-HFCTSLQGLGSIAGVMATLGYPLPQLPQTEP 167
Db 179 ERQIALHRSRPLRELYDEVA-----AYEPVPSVPGAEP 211

Search completed: August 10, 2004, 06:44:12
Job time : 14.5 secs

RESULT 13
B75332
extracellular solute-binding protein, family 5 - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: B75332
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:110567266
A:Accession: B75332
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-520 <WHI>
A:Cross-references: GB:AE002034; GB:AE000513; NID:G6459742; PIDN:AAF11508.1; PID:G645974
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1955
A:Map position: 1
C:Superfamily: dipeptide transport protein

Query Match 6.9%; Score 85; DB 2; Length 520;
Best Local Similarity 23.3%; Pred. No. 6.1;
Matches 40; Conservative 20; Mismatches 54; Indels 58; Gaps 7;
QY 19 LWHLPVAVPALNRTGDPGPGPSIQ-----KTYDLTRYLEHQLRSLAGTVLYN 63
Db 363 LWY-----PSISRNLYLPFKPVAEALADLGAIGIKVNLKTEDWPKYLEDRRAGVFQWLY 418
QY 64 YLGPFPNEPD-----FNPRPLGAEITLPRATVNLVWRSNL-DRRLTON 106
Db 419 GWGGDYNDPDNFYAFYDYGKSDDIGFNP-----NILNTLNKGRALTOA 464
QY 107 YEAYSHLLCYLRLNQRAATAELRRSLAHFCTSLQ-----LLGSIAGVMATLG 155
Db 465 QKA-----PYVQKHELTYNANVLPLVHSTAPAAARTYKVGWITGTLSTVG 511

RESULT 14
A83271
hypothetical protein PA2984 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 25-Aug-2003
C:Accession: A83271
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83271
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-741 <STO>
A:Cross-references: GB:AE004724; GB:AE004091; NID:99949083; PIDN:AAG06372.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2984
C:Superfamily: competence protein ComC

Query Match 6.9%; Score 84; DB 2; Length 741;
Best Local Similarity 26.2%; Pred. No. 12;
Matches 64; Conservative 13; Mismatches 81; Indels 86; Gaps 13;
QY 5 AGDSW-----GMLACLCTVWLHPVAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGT 60
Db 447 AAAAWSVALGMALC-----WLAPA-----GLP-----LRLGAA 477
QY 61 YLNYLGPFPNEPDNFNPRPLGAEITLPRATVNLVWRSNLDRRLTONYEAAYSHLLCYLRG 119

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OM protein - protein search, using sw model

Run on: August 10, 2004, 06:43:28 ; Search time 8 Seconds
(without alignments)
1464.473 Million cell updates/sec

Title: US-09-931-704-5
Perfect score: 1224
Sequence: 1 MDLRAGDSWGLACLTCLVLM.....KKKMQPPAASVTLLHLEAHGF 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217.5	17.8	204	1	CTF2 MOUSE
2	118.5	9.7	203	1	CTF1 RAT
3	110.5	9.0	203	1	CTF1 MOUSE
4	93	7.6	423	1	CST MOUSE
5	91.5	7.5	201	1	CTF1 HUMAN
6	91.5	7.5	455	1	CTF2 MOUSE
7	90	7.4	195	1	CNTF CHICK
8	88	7.2	1009	1	M2B2 HUMAN
9	86	7.0	619	1	NKX1 HUMAN
10	86	7.0	1313	1	MIPL SCHPO
11	85.5	7.0	560	1	PHAC_PSEOL
12	84.5	6.9	294	1	HOPK_RHOCA
13	80.5	6.6	995	1	M2B2 PIG
14	79.5	6.5	830	1	VFP3 HUMAN
15	79	6.5	291	1	YM32 MYCTU
16	79	6.5	1132	1	BAT3 HUMAN
17	79	6.5	1620	1	ALK HUMAN
18	78.5	6.4	571	1	ATKA MYCTU
19	78.5	6.4	1473	1	NALI HUMAN
20	78.5	6.4	1844	1	POLR_TMYV
21	78	6.4	422	1	Y140 HUMAN
22	78	6.4	427	1	RT65 MYXHA
23	78	6.4	515	1	YBLJ SCHPO
24	78	6.4	917	1	SVI STAM
25	78	6.4	917	1	SVI STAAU
26	77.5	6.3	572	1	STM AERPE
27	77.5	6.3	1182	1	HAIR MOUSE
28	77	6.3	2261	1	RPLP MUMPM
29	76.5	6.2	870	1	BCAL HUMAN
30	76.5	6.2	2390	1	SPCP HUMAN
31	76	6.2	372	1	CD14 RABIT
32	76	6.2	508	1	BGR1 RAT
33	76	6.2	1137	1	MSB1 YEAST

34	75.5	6.2	334	1	BC12 HUMAN
35	75.5	6.2	346	1	YG2Q YEAST
36	75.5	6.2	390	1	YL28 STRCO
37	75	6.1	296	1	RECO ANASP
38	75	6.1	343	1	DFRA SYN3
39	75	6.1	452	1	TLL DROME
40	75	6.1	552	1	MP22 MOUSE
41	75	6.1	715	1	PERE HUMAN
42	74.5	6.1	346	1	CNA1 SCHPO
43	74.5	6.1	1009	1	FAK2 HUMAN
44	74.5	6.1	1941	1	YRM8 CABEL
45	74.5	6.1	2388	1	SPCP RAT

ALIGNMENTS

RESULT 1					
CTF2 MOUSE					
ID	CTF2 MOUSE	STANDARD;	PRT;	204 AA.	
DT	P83714;	AC			
DT	15-MAR-2004 (Rel. 43, Created)				
DT	15-MAR-2004 (Rel. 43, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Cardiotrophin-2 precursor (CT-2).				
GN	CTF2.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Hasegawa M., Habu K., Adachi Y., Natori O.;				
RT	"Cardiotrophin-2 increases the platelet counts with splenomegaly in vivo."				
RL	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.				
CC	-!- FUNCTION: Increases the platelet count associated with splenomegaly.				
CC	-!- SUBCELLULAR LOCATION: Secreted (By similarity).				
CC	-!- SIMILARITY: Belongs to the IL-6 superfamily.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AB125661; BAD01485.1; --				
KW	Cytokine; Signal.				
FT	SIGNAL 1 22 POTENTIAL.				
FT	CHAIN 23 204 CARDIOTROPHIN-2.				
FT	CARBOHYD 44 44 N-LINKED (GLCNAC..) (POTENTIAL).				
SQ	SEQUENCE 204 AA; 22000 NW; B05566C1E7C3D9C0 CRC64;				
Query Match 17.8%; Score 217.5; DB 1; Length 204;					
Best Local Similarity 29.4%; Pred. No. 4.3e-13; Indels 35; Gaps 5;					
Matches 62; Conservative 32; Mismatches 82;					
QY	14	CLCTVWLHLPALNRTGDPGFGPSIQKTYLDTRYLEHQLRSLAGTYINLYLGPFPNPD	73		
Db	10	CLLSLL-----LPLSPRAPISEPSPIQAYSLALYMQNWSALLQTYLQHOGSPFSDPG	64		
QY	74	FNPPIRGHETLPRAVNLVWRSLNDRILRTONTYAYSHLLCYLR-----G	119		
Db	65	FSAPQLQLSTLPSAAVSFKTWHAMEDAERLSRAQAFALTQHLQLVGDOSYLNPGSPI	124		
QY	120	LNKQATAELRRLAHFCTSLQGLIGSLAGVMTATGYPLP--QPLPGTEPAWAPGPAHSD	177		
Db	125	LIAQLGAELR-----AQGLGNMAINTALGLPIPEEDTLGFVPCA-----SA	170		
QY	178	FLQKMDDFWLLKELQTLWLRSAKDFNRLKKK	208		


```

RX MEDLINE=20193614; PubMed=10727929;
RA Hirahara Y., Tsuda M., Wada Y., Honke K.;
RT "cDNA cloning, genomic cloning, and tissue-specific regulation of
RT mouse ceroidase sulfotransferase.";
RL Eur. J. Biochem. 267:1909-1917(2000).
EN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaado I., Pesole G., Quackenbush J.,
RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
EN
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
EN
RP FUNCTION.
RX MEDLINE=21927584; PubMed=11917099;
RA Honke K., Hirahara Y., Dupree J., Suzuki K., Popko B., Fukushima K.,
RA Fukushima J., Nagasawa T., Yoshida N., Wada Y., Taniguchi N.;
RT "Paranodal junction formation and spermatogenesis require
RT sulfoglycolipids.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4227-4232(2002).
CC
CC -!- FUNCTION: Catalyzes the sulfation of membrane glycolipids. Seems
CC to prefer beta-glycosides at the nonreducing termini of sugar
CC chains attached to a lipid moiety. Catalyzes the synthesis of
CC HSO3-3-galactosylceramide (sulfatide), a major lipid component of
CC the myelin sheath and of HSO3-3-monogalactosylalkylglycerol
CC (seminolipid), present in spermatozoa. Also acts on
CC lactosylceramide, galactosyl 1-alkyl-2-sn-glycerol and galactosyl
CC diacylglycerol (in vitro).
CC -!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a
CC galactosylceramide = adenosine 3',5'-bisphosphate +
CC galactosylceramide sulfate.
CC -!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate +

```

```

CC monogalactosylalkylglycerol = adenosine 3',5'-bisphosphate +
CC monogalactosylalkylglycerol sulfate.
CC -!- PATHWAY: Sphingolipid and glycerolipid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By
CC similarity).
CC -!- TISSUE SPECIFICITY: Expressed in brain, testis, kidney, stomach,
CC small intestine, liver, and lung. Not detected in heart, skeletal
CC muscle, and spleen.
CC -!- MISCELLANEOUS: Mice homozygous for a null mutation of the CST gene
CC display hindlimb weakness from week 6 of age and subsequently show
CC a pronounced tremor and progressive ataxia. Myelin vacuolation is
CC observed in the cerebellar white matter, diencephalon, brainstem
CC and spinal anterior column. Male mice were infertile due to a
CC blocked spermatogenesis.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB032940; BAA93009.1; -
CC EMBL; AB032939; BAA93008.1; -
CC EMBL; AK007645; BAB25160.1; -
CC EMBL; BC026806; AAB26806.1; -
CC MGD; MGI:1858277; Gcst.
CC GO; GO:0016021; C:integral to membrane; IC.
CC GO; GO:0001733; F:galactosylceramide sulfotransferase activity; IDA.
CC GO; GO:0006682; P:galactosylceramide biosynthesis; IDA.
CC GO; GO:0043552; P:myelination; IMP.
CC GO; GO:0007283; P:spermatogenesis; IMP.
CC TRANSFERASE; Transmembrane; Glycoprotein.
CC DOMAIN 1 12
CC TRANSMEM 13 35
CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC LUMENAL CATALYTIC (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC L -> P (IN REF. 2).
CC R -> Q (IN REF. 2).
CC E -> K (IN REF. 2).
CC F -> R (IN REF. 1).
CC R -> G (IN REF. 2).
CC I -> T (IN REF. 1).
CC SEQUENCE 423 AA; 48968 MW; FD54A1A71F4AE46 CRC64;
Query Match 7.6%; Score 93; DB 1; Length 423;
Best Local Similarity 23.1%; Pred. No. 0.42;
Matches 55; Conservative 22; Mismatches 65; Indels 96; Gaps 11;
QY 44 YDLTRYLEHQLRSAGTYINY---LGPP-----FNEP----- 72
DB 204 YDPSSYNAHYLRNLFFDLGYDSSLDPSAPRQVQBHILEVERFHLVLQYFDESVLRLR 263
QY 73 -----DFNPRLGAETLPRAVNLVWRSLNDRRLRLTONYEAYSHL 113
DB 264 ELLCWDLEDVLYFKLNARDSPVPLSGELYRRAT-----ANWLD--VRLYRHNFAFWR 317
QY 114 LCYLKGLNRQA-ATAELRRS---LAFTSTLQGLGSTA-----GVNATLGYYP 157
DB 318 KVEAFGRFMAREVAELRQANEHMRHICIDGQAVGAIEAIDQDSAMQPWQLGIKISILGN 377
QY 158 LPQPLPGTPEAWAPGPAHSDFLQKMDDFWLAKELQ-----TWLWRSKDFNR 204
DB 378 LKSI-----GPQHEQLCRRM-----LTPFQYLSDLGLANLWVTKLWFLKDFLR 422

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RESULT 5
CTFL HUMAN
ID CTFL HUMAN STANDARD; PRT; 201 AA.
AC Q16619;

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DT	01-NOV-1997 (Rel. 35, Created)	CTV2_MOUSE	STANDARD;	PRT;	455 AA.
DT	01-NOV-1997 (Rel. 35, Last sequence update)	AC	Q9CWV7; Q8R163;		
DT	28-FEB-2003 (Rel. 41, Last annotation update)	DT	10-OCT-2003 (Rel. 42, Created)		
DE	Cartotrophin-1 (CT-1).	DT	10-OCT-2003 (Rel. 42, Last sequence update)		
GN	CTFL.	DT	10-OCT-2003 (Rel. 42, Last annotation update)		
OS	Homo sapiens (Human).	DE	Protein C20orf162 homolog.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	GN	C20orf162.		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OS	Mus musculus (Mouse).		
OX	NCBI_TaxID=9606;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
RN	[1]	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RP	SEQUENCE FROM N.A.	OX	NCBI_TaxID=10090;		
RC	TISSUE=Heart;	RN	[1]		
RA	Pennica D., Swanson T.A., Shaw K.J., Kuang W.-J., Gray C.L.,	RP	SEQUENCE FROM N.A.		
RA	Beatty B.G., Wood W.I.;	RC	STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;		
RT	"Human cardiotorphin-1: protein and gene structure, biological and	RX	MEDLINE=21085660; PubMed=11217851;		
RT	binding activities, and chromosomal localization.";	RA	Kawai J., Shinsagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RL	Cytokine 8:183-189(1996).	RA	Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
CC	-!- FUNCTION: Induces cardiac myocyte hypertrophy in vitro. Binds to	RA	Aizawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,		
CC	and activates the ILST/gp130 receptor.	RA	Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,		
CC	-!- SUBCELLULAR LOCATION: Secreted.	RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
CC	-!- TISSUE SPECIFICITY: Highly expressed in heart, skeletal muscle,	RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
CC	prostate and ovary. Lower levels in lung, kidney, pancreas,	RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,		
CC	thymus, testis and small intestine. Little or no expression in	RA	Schrei L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
CC	brain, placenta, liver, spleen, colon or peripheral blood	RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
CC	leukocytes.	RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
CC	-!- SIMILARITY: Belongs to the IL-6 superfamily.	RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
CC		RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
CC	the European Bioinformatics Institute. There are no restrictions on its	RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
CC	use by non-profit institutions as long as its content is in no way	RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
CC	modified and this statement is not removed. Usage by and for commercial	RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RA	Hayashizaki Y.;		
CC		RT	"Function: annotation of a full-length mouse cDNA collection.";		
CC		RL	Nature 409:685-690(2001).		
CC		RN	[2]		
DR	EMBL; U43033; AAD12173.1; -	RP	SEQUENCE FROM N.A.		
DR	EMBL; U43031; AAD12173.1; JOINED.	RC	STRAIN=C57BL/6; TISSUE=Brain, and Kidney;		
DR	EMBL; U43032; AAD12173.1; JOINED.	RX	MEDLINE=22388257; PubMed=12477932;		
DR	EMBL; U43030; AAA85229.1; -	RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
DR	PIR; G02312; G02312.	RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,		
DR	Genew; HGNC:2499; CTFL.	RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
DR	MIM; 600435; -	RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
DR	GO; GO:0005576; C:extracellular; TAS.	RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
DR	GO; GO:0005146; F:leukemia inhibitory factor receptor binding; TAS.	RA	Datchenko L., Marudina K., Farmer A., Rubin G.M., Hong L.,		
DR	GO; GO:0002853; P:cell proliferation; TAS.	RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
DR	GO; GO:0007267; P:cell-cell signaling; TAS.	RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
DR	GO; GO:0007517; P:muscle development; TAS.	RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
DR	GO; GO:0007399; P:neurogenesis; TAS.	RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
DR	GO; GO:0008284; P:positive regulation of cell proliferation; TAS.	RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
KW	Cytokine; Polymorphism.	RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
FT	92 92 A -> T (in dbSNP:2234933).	RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
FT	VARIANT 92 92 /FTID=VAR 014938.	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
FT	SEQUENCE 201 AA; 21227 MW; 0235A/B5745F675F CRC64;	RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
SQ	Query Match 7.5%; Score 91.5; DB 1; Length 201;	RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,		
	Best Local Similarity 25.7%; Pred. No. 0.22;	RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;		
	Matches 45; Conservative 23; Mismatches 92; Indels 15; Gaps 5;	RT	"Generation and initial analysis of more than 15,000 full-length		
		RT	human and mouse cDNA sequences.";		
QY	40 IQKTYDLTYLEHQLSLAGTVLYLGPFPNPDNPPRLGATETPRATVNLVWRSND 99	RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
Db		CC	-!- SIMILARITY: Contains 1 SWIM-type zinc finger.		
QY	27 IRQTHSLAHLTKYAEQLQEVYVQGDGPFGLPSPPLPVLG-SAPASHAGLPVHE 85	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
Db		CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
QY	100 RLRLTQNZAYSHLLCYLRGLNRQA-----TAELESLAHFCTSLQGLGSIAGVMATL 154	CC	the European Bioinformatics Institute. There are no restrictions on its		
Db		CC	use by non-profit institutions as long as its content is in no way		
QY	86 RLRL--DAAALALPDLAVCERQALNPRLRLRLLEDAARQALGAVALAAL 143	CC	modified and this statement is not removed. Usage by and for commercial		
QY	155 GY-----PLQPLPCTEPANAPGPAHSDFLQKMDDFLLKELQTLWLRSAKPNRL 205	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
Db		CC			
QY	144 GAANRGFRAPPAATASA---ASATGVFPKVLGLRVGLYREWLRSRTGDLGQL 195	DR	EMBL; AK010358; BAB26878.1; -		
Db		DR	EMBL; BC025194; AAH25184.1; ALT_INIT.		
		DR	EMBL; BC046831; AAH46831.1; -		
		DR			
		RESULT 6			


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DR MGI:1919221; 2410003H12Rik.
DR InterPro; IPR007527; Znf_SWIM.
DR Pfam; PF04434; SWIM; 1.
KW Zinc-finger.
FT ZN FING 342 375 SWIM-TYPE.
SQ SEQUENCE 455 AA; 51481 MW; 20188688.4EB9CFF CRC64;

Query Match
Best Local Similarity 7.5%; Score 91.5; DB 1; Length 455;
Matches 59; Conservative 21; Mismatches 75; Indels 95; Gaps 14;

QY 7 DSWGMLAGLCIVLW-HLPAVALARTGDPG-----PPSOKTYDLTRYLHQLRS 56
DQ 29 DAFNQSCFMQDLFAHFBEVLFIHRTYINPRGKLVYTFVLDGPRVQVEGLARAV----- 82
QY 57 LAGTYLNYLGGPFNE-----PDFNPPRLGAEITLPRATVNLVWRSNDRLRLT 104
DQ 83 -----YFAIPTNEDARGLAQMFQVKKFN-----AMERVNTIL--- 116
QY 105 QNYEAYSHLLCYLRGLNQAAAEARRSLAHFCTSLQ-----LLGSIAGV 150
DQ 117 ----VDPHFL-LLPTLTNFEPTAEYLLSAFHICKFLQCKFYQLFQVQRLILLSLQST 171
QY 151 M--ATLG-----YLPQLPGLTEPAWAPGPAHSDFLOKMDDFLLKELQTLW---WESAK 200
DQ 172 MCSATAGNLRLKLYL---LNNCIP-----SSRLPELHSHWLND-RIWLAHRWSRA 219
QY 201 DFNRLKXMQ 210
DQ 220 QSSRYFQSLQ 229

RESULT 7
CNTF_CHICK STANDARD; PRT; 195 AA.
ID CNTF_CHICK
AC Q02011;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Ciliary neurotrophic factor (CNTF) (Growth promoting activity) (GPA).
GN CNTF OR GPA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RX MEDLINE=92304573; PubMed=1610564;
RA Leung D.W., Parent A.S., Cachianes G., Lee A.L., Nikolics K.,
RA Esch F., Coulombe J.N., Blacher R.W., Eckenstein F.P., Nishi R.;
RT "Cloning, expression during development, and evidence for release of
RT a trophic factor for ciliary ganglion neurons."
RL Neuron 8:1045-1053(1992).
CC -!- FUNCTION: CNTF is a survival factor for various neuronal cell
CC types. Seems to prevent the degeneration of motor axons after
CC axotomy.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Nervous system.
CC -!- SIMILARITY: Belongs to the CNTF family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M80827; AAA48784.1; -
CC PIR; JH0680; JH0680.
CC HSSP; P26441; 1CNT.
CC InterPro; IPR000151; Cil_neuro_factor.

DR MGI:1919221; 2410003H12Rik.
DR InterPro; IPR007527; Znf_SWIM.
DR Pfam; PF04434; SWIM; 1.
KW Zinc-finger.
FT ZN FING 342 375 SWIM-TYPE.
SQ SEQUENCE 455 AA; 51481 MW; 20188688.4EB9CFF CRC64;

Query Match
Best Local Similarity 7.4%; Score 90; DB 1; Length 195;
Matches 52; Conservative 21; Mismatches 83; Indels 32; Gaps 10;

QY 46 LTRYLHQLRSAGTYLNLVILGPPNPDFFNPPRLGAEITLPRATVNLVWRSNDRLRLTQ 105
DQ 23 LARKMSDVTDLDDIIVVERQG-----LDASISVAADVGVPTAAV--ERNAEQTGTRQLLD 75
QY 106 N---ZEAYSHLLCYLRGLNRQA---ATAELRRSLA-----HFCTSLQGLLSIAGVMA 152
DQ 76 NLAAYRAFRLLAQMLEEQRELLGDTDAELGPALAAWLLQVSAFVHLSELL-----ELE 130
QY 153 TLGYPLPQLPGLTEPAWAPGPAHSDFLOKMDDFLLKELQTLWRSKAFNRLKKMQDP 212
DQ 131 SRGAPAE--GSEPP-AP-PRLSLFEQKRLGLRLVRLAQWAVRSVRDLRLQLSK--HGP 183
QY 213 AASVTLHL 220
DQ 184 GSGAALGL 191

RESULT 8
M2B2 HUMAN STANDARD; PRT; 1009 AA.
ID M2B2 HUMAN
AC Q9Y2E5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Epididymis-specific alpha-mannosidase precursor (EC 3.2.1.24)
DE (Mannosidase alpha class 2B member 2).
GN MAN2B2 OR KIAA0935.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Stone N.E., Schmutz J.J., Cox D.R., Myers R.M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]_TaxID=9606;
RP SEQUENCE OF 132-1009 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99246083; PubMed=10231032;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 6:63-70(1999).
RN [3]_TaxID=9606;
RP RECONSTRUCTION FROM GENOMIC SEQUENCE.
RA Bairoch A.;
CC Unpublished observations (NOV-2001).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing alpha-D-
CC mannose residues in alpha-D-mannosides.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: Belongs to family 38 of glycosyl hydrolases.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AC004480; -; NOT ANNOTATED CDS.
CC EMBL; AB023152; BAA76779.1; ALT_SEQ.
CC
CC DR MGI:1919221; 2410003H12Rik.
CC DR InterPro; IPR007527; Znf_SWIM.
CC DR Pfam; PF04434; SWIM; 1.
CC KW Zinc-finger.
CC FT ZN FING 342 375 SWIM-TYPE.
CC SQ SEQUENCE 455 AA; 51481 MW; 20188688.4EB9CFF CRC64;
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DR InterPro; IPR000602; Glyco_hydro_38.
 DR Pfam; PF01074; Glyco_hydro_38; 1.
 KW Hydrolase; Glycosidase; Signal; Glycoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 1009 EPIDIDYMIS-SPECIFIC ALPHA-MANNOSIDASE.
 FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 516 516 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 670 670 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 808 808 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 890 890 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1009 AA; 113987 MW; F3DB81DD061352E6 CRC64;
 Query Match 7.2%; Score 88; DB 1; Length 1009;
 Best Local Similarity 23.3%; Pred. No. 3.7;
 Matches 45; Conservative 21; Mismatches 65; Indels 62; Gaps 8;
 QY 50 LEHQ-----LRSLAGTYLVLPFPNPPRLGAEITPRATVNVLRVSRINDRLRLTQ 105
 Db 842 LQHRPVVFGDLGATAPKLPFGQQEAVTLPPNHLQL-----SIPGWRYSNHTHSQ 896
 QY 106 NYEAYSHLLCYLRLNRQATRLRLSLAHF-----CTSLQGLLSIAG 149
 Db 897 N-----LRKGRGEQAQDLRLRLRLYHLVEGSDPVLSQPVTVNLQVLAQLGS 946
 QY 150 VMATLCPVLPQPLPGTEPAWAPGPAHSDFLQKMDPFLKKEQLTWLRSAKDFNR--LKK 207
 Db 947 VVAV-----EERSUTGT-----WDLMLRLHRSWRTGPGHGRDITS 982
 QY 208 KMOPPAAS-VTLH 219
 Db 983 PSRPFGGPIITVH 995
 RESULT 9
 NXF1 HUMAN STANDARD; PRT; 619 AA.
 AC Q9UBU9; Q9UBU9; Q9UOL2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Nuclear RNA export factor 1 (tip associating protein) (Tip-associated
 DE protein) (mRNA export factor TAP).
 GN NXF1 OR TAP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=99219873; PubMed=10202158;
 RA Braun I.C., Rohrbach E., Schmitt C., Izaurralde E.;
 RT "RAP binds to the constitutive transport element (CTE) through a novel
 RT RNA-binding motif that is sufficient to promote CTE-dependent RNA
 RT export from the nucleus.";
 RL EMBO J. 18:1953-1965 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99257272; PubMed=10323864;
 RA Kang Y., Cullen B.R.;
 RT "The human Tap protein is a nuclear mRNA export factor that contains
 RT novel RNA-binding and nucleocytoplasmic transport sequences.";
 RL Genes Dev. 13:1126-1139 (1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99384298; PubMed=10454577;
 RA Bear J., Tan W., Zolotukhin A.S., Tabernero C., Hudson E.A.,
 RA Feiber B.K.;
 RT "Identification of novel import and export signals of human TAP, the
 RT protein that binds to the constitutive transport element of the type
 RT D retrovirus mRNAs.";
 RL Mol. Cell. Biol. 19:6306-6317 (1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Lung;
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
 RA Oabayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
 RA Iscgai T., Sugano S.;
 RT "REDU human cDNA sequencing project.";
 RL Nucleic Acids Res. 27:115-116 (1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain, and Placenta;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
 RN [6]
 RP SEQUENCE OF 61-619 FROM N.A.
 RX TISSUE=Lymphocytes;
 RA MEDLINE=97318898; PubMed=9175835;
 RA Yoon D.-W., Lee H., Seol W., Demaria M., Rosenzweig M., Jung J.U.;
 RT "Tap: a novel cellular protein that interacts with tip of herpesvirus
 RT saimiri and induces lymphocyte aggregation.";
 RL Immunity 6:571-582 (1997).
 RN [7]
 RP FUNCTION.
 RX MEDLINE=98325379; PubMed=9660949;
 RA Grueter P., Tabernero C., von Kobbe C., Schmitt C., Saavedra C.,
 RA Bachi A., Wilim M., Felber B.K., Izaurralde E.;
 RT "TAP, the human homolog of Mex67p, mediates CTE-dependent RNA export
 RT from the nucleus.";
 RL Mol. Cell 1:649-659 (1998).
 RN [8]
 RP CHARACTERIZATION.
 RX MEDLINE=21282872; PubMed=11259411;
 RA Braun I.C., Herold A., Rode M., Conti E., Izaurralde E.;
 RT "Overexpression of TAP/p15 heterodimers bypasses nuclear retention and
 RT stimulates nuclear mRNA export.";
 RL J. Biol. Chem. 276:20536-20543 (2001).
 RN [9]
 RP CHARACTERIZATION.
 RX MEDLINE=20132240; PubMed=10668806;
 RA Bachi A., Braun I.C., Rodrigues J.P., Pante N., Ribbeck K.,
 RA von Kobbe C., Kutay U., Wilim M., Gorlich D., Carmo-Fonseca M.,
 RA Izaurralde E.;
 RT "The C-terminal domain of TAP interacts with the nuclear pore complex
 RT and promotes export of specific CTE-bearing RNA substrates.";
 RL RNA 6:136-158 (2000).
 RN [10]

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Mousle S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds R., Squares R., Squares S., Stevens K.,
 RA Taylor K., Tivey R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkhaert G., Aert R., Robben J., Grymonprez B.,
 RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moesti D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Fuelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:871-880(2002).
 CC -!- FUNCTION: BINDS TO AND FACILITATES THE FUNCTIONING OF THE MEIOTIC
 CC REGULATOR MEI2. MAY ALSO BE INVOLVED IN CONJUGATION BY INTERACTING
 CC WITH STE11. ESSENTIAL FOR CELL GROWTH.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Contains 7 WD repeats.
 CC
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 CC
 CC EMBL; AB032552; BAA84585.1; -.
 CC EMBL; Z95396; CAB08769.1; -.
 CC PIR; T38943; T38943.
 CC GeneDB: Spombe; SPAC57A7.11; -.
 CC InterPro: IPR008938; ARM.
 CC InterPro: IPR001680; WD40.
 CC InterPro: IPR004083; Yeast176.
 CC Pfam; PF00400; WD40; 5
 CC PRINTS; PR01547; YEAST176DUF.
 CC SMART; SM00320; WD40; 6.
 CC PROSITE; PS00678; WD_REPEATS_1; 1.
 CC PROSITE; PS00682; WD_REPEATS_2; 2.
 CC PROSITE; PS50294; WD_REPEATS_REGION; 1.
 CC Meiosis; WD repeat; Repeat.
 CC REPEAT 986 1029 WD 1.
 CC REPEAT 1033 1074 WD 2.
 CC REPEAT 1087 1126 WD 3.
 CC REPEAT 1130 1170 WD 4.
 CC REPEAT 1176 1216 WD 5.
 CC REPEAT 1219 1259 WD 6.
 CC REPEAT 1268 1308 WD 7.
 CC SEQUENCE 1313 AA; 148533 MW; C71B663B0171E7A4 CRC64;
 Query Match 7.0%; Score 86; DB 1; Length 1313;
 Best Local Similarity 22.2%; Pred. No. 7.9;
 Matches 58; Conservative 31; Mismatches 84; Indels 85; Gaps 12;
 QY 15 LCTVLMHLPVAV--PALNR-----TGDPGPGPSI-----OKTYDLTRYLHQLRS 56
 DB 811 LAFLLQHLPAHKASLSKDTNSVTSDPKPHFPVPSVSENKILNRSFSLTRSLKGLALS 870
 QY 57 LAG-----TYVNYL-----GPP-FNEPDFNPPRLCAETLPATVNL 91
 DB 871 LAGSDRASSELLSLNGENKPAESNLNLTSAKVPGPAPFAFNELEYQ-----SELDMPITYLF 926
 QY 92 EVWRSNDRLRLRLQNYEAYSHLLCYLRLGL---NRQAATAELRLSLAHFCTS-----LQG 142

DB 927 DWSRKFTYFPQRPNEDEDDPFGICYNQRLRRNRNEKLIYRTRPLAAYSTNGRWNOQLMT 986
 QY 143 LLGSIAGVWATLGYPLPQPLPGTEPAWAPGPAHSDFLQKDDDFLLKE---LQTLWLSA 199
 DB 987 FNTTIA-----PRKLMPHQEDQLITLGDKDIIVWDREN 1022
 QY 200 KDFNRLKKMQPPPAASVTLHL 220
 DB 1023 RCLNSFK-----TSASATTNV 1038
 RESULT 11
 PHAC PSEOL STANDARD; PRT; 560 AA.
 AC P26456;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Poly(3-hydroxyalkanoate) polymerase 2 (EC 2.3.1.-) (PHA polymerase 2)
 DE (PHA synthase 2) (polyhydroxyalkanoic acid synthase 2).
 OS Pseudomonas oleovorans.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=301;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GP01;
 RC MEDLINE=91115830; PubMed=1989978;
 RA Huismann G.W., Wonink B., Meima R., Kazemier B., Terpstra P.,
 RA Witholt B.;
 RA "Metabolism of poly(3-hydroxyalkanoates) (PHAs) by Pseudomonas
 RT oleovorans. Identification and sequences of genes and function of the
 RT encoded proteins in the synthesis and degradation of PHA";
 RL J. Biol. Chem. 266:2191-2198(1991).
 CC -!- FUNCTION: P. OLEOVARANS ACCUMULATES POLY(3-HYDROXYALKANOATES) AFTER
 CC GROWTH ON MEDIUM CHAIN LENGTH HYDROCARBONS. LARGE AMOUNTS OF TH-S
 CC POLYESTER ARE SYNTHESIZED WHEN CELLS ARE GROWN UNDER NITROGEN-
 CC LIMITING CONDITIONS. WHEN NITROGEN IS RESUPPLIED IN THE MEDIUM,
 CC THE ACCUMULATED PHA IS DEGRADED.
 CC -!- SIMILARITY: Belongs to the PHA/PHB synthase family.
 CC
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 CC
 CC EMBL; M58445; AAA25934.1; -.
 CC PIR; C38604; C38604.
 CC InterPro: IPR000073; A/b hydrolase.
 CC Pfam; PF00561; abhydrolase_1; Acyltransferase.
 CC PHA biosynthesis; transferase; 296
 CC ACT SITE 296 POTENTIAL.
 CC SEQUENCE 560 AA; 62631 MW; E2CD844FC1616B83 CRC64;
 Query Match 7.0%; Score 85.5; DB 1; Length 560;
 Best Local Similarity 30.2%; Pred. No. 3;
 Matches 38; Conservative 16; Mismatches 43; Indels 29; Gaps 7;
 QY 77 PRCAETLPATVNLVWRSNDRRLRLTQNYEAYSHLLCYLRLNQCAETARRSI--A 134
 DB 5 PAKGTPLTPATSMNVQ-----NAILGRGR-----DLISLRNVSRQS-----LRHPLHTA 50
 QY 135 HFCTSLQGLGSLAGVWATLGYPLPQPLPG-----TEPAWAPGPAHSDFLQKDDDFLLKE 190
 DB 51 HLLIALGGQLGRV-----ILGDTPLQNPDPFSDPTWSONPFYRRLQA-----YLAWQ 101
 QY 191 LQTLW 196

```
Db 102 KQRLW 107
RESULT 12
HUPK_RHOCA
ID HUPK_RHOCA STANDARD; PRT; 294 AA.
AC P30797;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hydrogenase expression/formatation protein hupK.
GN HUPK.
OS Rhodobacter capsulatus (Rhodopseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A. PubMed=2007559;
RX MEDLINE=91177833;
RA Xu H.W., Wall J.D.;
RT "Clustering of genes necessary for hydrogen oxidation in Rhodobacter
RT capsulatus."
RN J. Bacteriol. 173:2401-2405(1991).
EN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33303 / B10;
RX MEDLINE=93268090; PubMed=8497190;
RA Colbeau A., Richard P., Toussaint B., Caballero F.J., Elster C.,
RA Delphin C., Smith R.L., Chabert J., Vignais P.M.;
RT "Organization of the genes necessary for hydrogenase expression in
RT Rhodobacter capsulatus." Sequence analysis and identification of two
RT hyp regulatory mutants."
RL Mol. Microbiol. 8:15-29(1993).
CC -! SIMILARITY: Belongs to the hupK family.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; M55089; AAA72924.1; -
DR EMBL; Z15089; CAA78803.1; -
DR PIR; S32947; S32947.
FT CONFLICT 70 70 A -> R (IN REF. 2).
SQ SEQUENCE 294 AA; 30222 MW; 2669E8B70AF35EDA CRC64;

Query Match 6.9%; Score 84.5; DB 1; Length 294;
Best Local Similarity 31.2%; Pred. No. 1.6;
Matches 40; Conservative 3; Mismatches 38; Indels 47; Gaps 6;

QY 76 PPRGAEPLPRATVNVLRSLNDRLTQNYEAYSHLLCYLRGLNQAAATAE---LRRS 132
Db 36 PPGQVAELLPR-----LFNLGAAQGHAAALAL-----GLPAEAPARREILRDH 80
QY 133 LAHFCTSLQGLGSLAGWATIGYLPPLPCTEPAWAPGPAHSDFLQKDDFWLLKELQ 192
Db 81 LAKLCLWPKLLGL-----APQPLP---EHWAEGA-----ALQ 111
QY 193 TWLWRSK 200
Db 112 HNLWGAK 119

RESULT 13
M2B2_PIG
ID M2B2_PIG STANDARD; PRT; 995 AA.
AC Q28949;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Epididymis-specific alpha-mannosidase precursor (EC 3.2.1.24)
DE (Mannosidase alpha class 2B member 2) (AWAN).
GN YAN2B2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE=Epididymis;
RX MEDLINE=96117077; PubMed=8562059;
RA Okamura N., Tamba M., Liao H.-J., Onoe S., Sugita Y., Dacheux F.,
RA Dacheux J.-L.;
RT "Cloning of complementary DNA encoding a 135-kilodalton protein
RT secreted from porcine corpus epididymis and its identification as an
RT epididymis-specific alpha-mannosidase."
RL Mol. Reprod. Dev. 42:141-148(1995).
CC -! FUNCTION: CAN DIGEST BOTH P-NITRO-PHENYL-ALPHA-D-MANNOSIDE AND
CC HIGH MANNOSE OLIGOSACCHARIDE (MAN(8)-GLCNAC(2)). MAY BE INVOLVED
CC IN SPERM MATURATION. HAS A POSSIBLE ROLE IN SPECIFIC SPERM-EGG
CC INTERACTION SINCE SPERM SURFACE MANNOSIDASE ACTS LIKE A RECEPTOR
CC FOR MANNOSE-CONTAINING OLIGOSACCHARIDES LOCATED ON THE ZONA
CC PELLUCIDA.
CC -! CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing alpha-D-
CC mannose residues in alpha-D-mannosides
CC -! SUBCELLULAR LOCATION: SECRETED. FOUND AT THE SPERM SURFACE AS A
CC 27 kDa FRAGMENT.
CC -! TISSUE SPECIFICITY: SPECIFIC TO THE CAPUT AND CORPUS OF THE
CC EPIDIDYMIS.
CC -! PTM: PROCESSED INTO A 27 kDa FRAGMENT LOCALIZED ON THE EQUATORIAL
CC SEGMENT AND THE APICAL RIM OF THE HEAD OF MATURE SPERM.
CC -! MISCELLANEOUS: OPTIMAL MANNOSIDASE ACTIVITY WAS FOUND AT PH 6.5.
CC -! SIMILARITY: Belongs to family 38 of glycosyl hydrolases.
CC -----
DR EMBL; D28521; BAA05877.1; ALT INIT.
DR InterPro; IPR000602; Glyco_hydro_38; 1_38.
DR Pfam; PF01074; Glyco_hydro_38; 1_38.
KW Hydrolase; Glycosidase; Signal; Glycoprotein.
FT SIGNAL 1 21
FT CHAIN 22 995 EPIDIDYMIS-SPECIFIC ALPHA-MANNOSIDASE.
FT CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 593 593 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 657 657 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 733 733 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 793 793 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 875 875 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 977 977 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 945 945 D -> A (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 995 AA; 114230 MW; 79D21B8C5A66FC2 CRC64;

Query Match 6.8%; Score 80.5; DB 1; Length 995;
Best Local Similarity 23.0%; Pred. No. 18;
Matches 45; Conservative 22; Mismatches 62; Indels 67; Gaps 9;

QY 50 LEHQ-----LRSAGTYLVNLPFPNPFNPPRPLGAETL-----PRATVNVLRSL 97
Db 827 LQRPVVLRELGGTVQNGFGPKQEPVTLPSHLQILSIQWKYSSNHTVHLKLNQKG 886
QY 98 NDR-----LRLTONYAYSHLLCYLRGLNQAAATAEILRRSLAHFCTSLQGLGSI 147
Db 887 HYRRKADFRVLLRLHLHLYEAGEH-----QALSREPVT-----LNLQSVLRGL 929
QY 148 AGYMATIGYLPPLPCTEPAWAPGPAHSDFLQKDDFWLLKELQTLWMSAKDFNR--L 205
```

Db 930 GSVAV-----ERSLTGT-----WDVNSLHRWSWKTDGHHHRGS 965
QY 206 KKKMQPP--AASVTLH 219
Db 966 SRRLPLRGPVTH 981

RESULT 14
VPP3 HUMAN
ID VPP3 HUMAN STANDARD; PRT; 830 AA.
AC Q13488; 075877;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Vacuolar proton translocating ATPase 116 kDa subunit a isoform 3 (V-ATPase 116-kDa isoform a3) (Osteoclastic proton pump 116 kDa subunit) (OC-116 kDa) (OC116) (T-cell immune regulator 1) (T cell immune response cDNA7 protein) (TIRC7).
GN TCIRG1 OR ATP6V0A3 OR ATP6NIC.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC TISSUE=Osteoclastoma;
RX MEDLINE=96158968; PubMed=8579597;
RA Li Y.P., Chen W., Stashenko P.;
RT "Molecular cloning and characterization of a putative novel human osteoclast-specific 116-kDa vacuolar proton pump subunit.";
RL Biochem. Biophys. Res. Commun. 218:813-821(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RA Utku N., Heinemann T., Bulwin C.-G., Beinke S., Beato F., Randall J., Busconi L., Delphire E., Robertson E.R., Kojima R., Volk H.D., Milford E.L., Gullans S.R.;
RA "Genomic organization of the gene coding for TIRC7, a novel membrane protein essential for T cell activation.";
RL Genomics 57:398-406(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=99263502; PubMed=10329006;
RA Heinemann T., Bulwin C.C., Randall J., Schnieders B., Sandhoff K., Volk H.D., Milford E., Gullans S.R., Utku N.;
RA "Genomic organization of the gene coding for TIRC7, a novel membrane protein essential for T cell activation.";
RL Genomics 57:398-406(1999).
CC -!- FUNCTION: PART OF THE PROTON CHANNEL OF V-ATPASES (BY SIMILARITY).
CC SEEMS TO BE DIRECTLY INVOLVED IN T CELL ACTIVATION.
CC -!- SUBUNIT: The V-ATPase is an heteromultimeric enzyme composed of at least thirteen different subunits. It has a membrane peripheral V1 sector for ATP hydrolysis and an integral V0 for proton translocation. The V1 sector comprises subunits A-H, whereas V0 includes subunits a, d, c', and c''.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q13488-1; Sequences=Displayed;
CC Name=Short;
CC IsoId=Q13488-2; Sequences=VSP_000345;
CC Notes=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: The long isoform is highly expressed in osteoclastomas. The short isoform is highly expressed in thymus.
CC -!- SIMILARITY: Belongs to the V-ATPase 116 kDa subunit family.
CC -----
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CC -----
CC EMBL; U45285; AAA97878.1; -.

DR EMBL; AF025374; AAC35742.1; -.
DR EMBL; AF033033; AAD31081.2; -.
DR Genew; HGNC:11647; TCIRG1.
DR MIM; 604592; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005215; P:transporter activity; TAS.
DR GO; GO:0006988; P:cellular defense response; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR GO; GO:0015992; P:proton transport; TAS.
DR InterPro; IPR002490; V_ATPase_sub116.
DR Pfam; PF01496; V_ATPase_sub_a; 1.
KW Hydrogen ion transport; Transmembrane; Glycoprotein;
KW Alternative splicing.
FT DOMAIN 1 397 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 398 418 POTENTIAL.
FT TRANSMEM 445 465 POTENTIAL.
FT TRANSMEM 504 524 POTENTIAL.
FT TRANSMEM 538 558 POTENTIAL.
FT TRANSMEM 576 596 POTENTIAL.
FT TRANSMEM 636 656 POTENTIAL.
FT TRANSMEM 771 791 POTENTIAL.
FT CARBOHYD 41 41 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 483 483 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 503 503 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 1 216 Missing (in isoform Short).
FT FTid=VSP_000345.
FT CONFLICT 377 377 A -> R (IN REF. 1).
FT CONFLICT 603 603 MISSING (IN REF. 1).
SQ SEQUENCE 830 AA; 92997 MW; 62EAE9A22DC698B CRC64;
Query Match 6.5%; Score 79.5; DB 1; Length 830;
Best Local Similarity 24.3%; Pred. No. 18;
Matches 45; Conservative 25; Mismatches 66; Indels 49; Gaps 9;
QY 40 IQKTYDITRVLEHQRLSLAGTYLVNLCPPNEFDNPPRLGATLTLPATVNVLEWRLND 99
Db 61 LKTF---TFLQEVRR-AGL---VLPFPKGRULPAPPFR-----D 93
QY 100 LRLTQNYEAYSHLLCYLRGLNRQAATAELRRSLAHFCTSLQGLGSIAGVM---ATLGY 156
Db 94 LLRIQETETERLAQELRDVRG-NQALRAQLHQLHAAVLROGHEPQLAAAHDTGASERT 152
QY 157 PLQPLPGTEPAWAPGPAHSD----FLQKDDFWLLKELQTLWRSKAK-----DFNRLKK 207
Db 153 PLLQ-----APGPHQDLRVNFVAGAVEPHKAPALERLLWRACROFLIASFRELEQ 203
QY 208 KMOPP 212
Db 204 PLEHP 208
RESULT 15
YM32 MYCTU
ID YM32 MYCTU STANDARD; PRT; 291 AA.
AC Q10515; Q10516;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein RV2232/RV2233/MT2292/MB2257.
GN RV2232/RV2233 OR MT2292 OR MTCY427.13/MTCY427.14 OR MB2257.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

Job time : 10 secs

```
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.P., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrett B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
CC -!- SIMILARITY: Belongs to the cbbY/cbbZ/gph/yieH family.
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CC -----
DR EMBL; Z70692; CAA94666.1; ALT TERM.
DR EMBL; Z70692; CAA94665.1; ALT INIT.
DR EMBL; AE007074; AAK46576.1; -.
DR EMBL; BX248341; CAD97110.1; -.
DR TIGR; MT2292; -.
DR Tuberculist; RV2232; -.
DR Tuberculist; RV2233; -.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00702; Hydrolase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 291 AA; 30694 MW; 750F090FB154E6E5 CRC64;
```

Query Match 6.5%; Score 79; DB 1; Length 291;
Best Local Similarity 25.8%; Pred. No. 5.2;
Matches 47; Conservative 16; Mismatches 65; Indels 54; Gaps 11;

QY 23 PAVPALNRTGPGPGPSIQKTYDLYRYLHQLRSLAGTY---LNYLGPPNPPDF----- 74
Db 64 PPRAAARASPGSPQI-VIFDLDTLDSARGIVSFRHNLNHGAPVPEGDLATHIV 122
QY 75 NPPRLGAEITLP-----RATVNLVYVRSINDRLRLTQNVAYSHLLCYLR- 118
Db 123 GPPM--HETLRANGIGESAEAEIYAYRADYSARGW-----ANNSLFDGIGPLADLRT 173
QY 119 -GLNRQAATAE-----LRSLAHF-----CTSLQGLGSIAGVATIGYPLPQ--P 161
Db 174 AGVRLAVATSKAEPTRARILRHFGIEQHFEVIAGASTDGRSGKVDVLA---HALAQLRP 230
QY 162 LP 163
Db 231 LP 232

Search completed: August 10, 2004, 06:46:28

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OM protein - protein search, using sw model

Run on: August 10, 2004, 06:43:28 ; Search time 35 Seconds
(without alignments)
2028.331 Million cell updates/sec

Title: US-09-931-704-5

Perfect score: 1224

Sequence: 1 MDLRAGDSWGMCLCTVLM.....KKKMQPPAASVTLHLEAGF 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rhodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1224	100.0	225	11 Q9QZM3	Q9QZM3 mus musculus
2	1193	97.5	225	4 Q9UBD9	Q9UBD9 homo sapien
3	144.5	11.8	215	13 Q9PUJ1	Q9PUJ1 plethodon j
4	144.5	11.8	215	13 Q9PUU0	Q9PUU0 plethodon j
5	144.5	11.8	215	13 Q9PUJ2	Q9PUJ2 plethodon j
6	142.5	11.6	215	13 Q9PUJ9	Q9PUJ9 plethodon j
7	109	8.9	471	16 Q8AR4	Q8AR4 pseudomonas
8	94	7.7	287	4 Q8N358	Q8N358 homo sapien
9	94	7.7	8601	2 Q8GM87	Q8GM87 symbiont ba
10	93.5	7.6	640	16 Q54153	Q54153 streptomyce
11	93	7.6	727	11 Q88841	Q88841 mus musculus
12	92.5	7.6	200	16 Q8YB1	Q8YB1 bruceella me
13	92.5	7.6	232	16 Q8FX31	Q8FX31 bruceella su
14	92.5	7.6	243	4 Q8NEV9	Q8NEV9 homo sapien
15	92.5	7.6	860	16 Q82G16	Q82G16 streptomyce
16	92	7.5	332	10 Q9MAU1	Q9MAU1 arabidopsis

17	92	7.5	555	11 Q8BY35	Q8BY35 mus musculus
18	90	7.4	733	16 Q8HIC5	Q8HIC5 pseudomonas
19	89.5	7.3	379	2 Q8KRX4	Q8KRX4 streptomyce
20	89.5	7.3	530	3 Q8XOE9	Q8XOE9 neurospora
21	89	7.3	733	16 Q91664	Q91664 pseudomonas
22	88	7.2	222	2 Q91584	Q91584 streptococ
23	88	7.2	1024	16 Q8XS09	Q8XS09 raietonia s
24	87	7.1	392	2 Q8KNF2	Q8KNF2 micromonospp
25	86.5	7.1	385	16 Q8ZM00	Q8ZM00 streptomyce
26	86.5	7.1	318	4 Q96LS2	Q96LS2 homo sapien
27	85.5	7.0	389	17 Q9YA71	Q9YA71 aeropyrum p
28	85.5	7.0	522	7 Q8HWH4	Q8HWH4 mus musculus
29	85.5	7.0	1122	10 Q8GVQ8	Q8GVQ8 oryza sativ
30	85.5	7.0	1154	11 Q921R2	Q921R2 mus musculus
31	85	6.9	392	11 Q8B113	Q8B113 mus musculus
32	85	6.9	422	11 Q8BGR5	Q8BGR5 mus musculus
33	85	6.9	476	11 Q8R363	Q8R363 mus musculus
34	85	6.9	520	16 Q9RT14	Q9RT14 deinococcus
35	85	6.9	585	5 Q9VNR6	Q9VNR6 drosophila
36	85	6.9	1009	4 Q8GT67	Q8GT67 homo sapien
37	85	6.9	1024	16 Q8FRH1	Q8FRH1 corynebacte
38	84.5	6.9	716	16 Q8PI99	Q8PI99 xanthomonas
39	84	6.9	468	16 Q8DHQ5	Q8DHQ5 synecococc
40	84	6.9	741	16 Q9HZM0	Q9HZM0 pseudomonas
41	83	6.8	272	16 Q86721	Q86721 streptomyce
42	83	6.8	396	2 Q9AF00	Q9AF00 frankia sp.
43	83	6.8	456	13 Q8AYL4	Q8AYL4 oncorhynch
44	83	6.8	955	11 Q88287	Q88287 mus musculus
45	83	6.8	982	11 Q7TSJ4	Q7TSJ4 mus musculus

ALIGNMENTS

RESULT 1

Q9QZM3 PRELIMINARY; PRT; 225 AA.
 ID Q9QZM3
 AC Q9QZM3
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Neurotrophin-1/B-cell stimulating factor-3.
 GN BSF3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99432284; PubMed=10500198;
 RA Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S.,
 RA Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Manu F.,
 RA Simonet W.S., Boone T., Chang M.-S.;
 RT "Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the
 RT IL-6 family";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).
 DR EMBL; AFI16913; AAF00993.1; -;
 DR MGD; MGI:1930088; Bsf3.
 DR GO; GO:0005125; F:cytokine activity; IDA.
 DR GO; GO:0030183; P:B-cell differentiation; IDA.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IDA.
 DR GO; GO:0007259; P:JAK-STAT cascade; IDA.
 SQ SEQUENCE 225 AA; 25261 MW; 68B1FEAB7F1A950 CRC64;

Query Match 100.0%; Score 1224; DB 11; Length 225;
 Best Local Similarity 100.0%; Pred. NO. 2e-108;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLRAGDSWGMCLCTVLMHLPVAPALNRTGDPGPSIQKTYLDTLYLEHQLRLAGT 60

Db 1 MDLRAGDSWGMCLCTVLMHLPVAPALNRTGDPGPSIQKTYLDTLYLEHQLRLAGT 60

Qy 61 YLNYLGPPFNEPDNPPRLGAETPLPRATVNVLRSLNDRILRTQNYEAYSHLLCYLRGL 120

Db 61 YLNYLGPPNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTQNYEAYSHLLCYLRGL 120
 QY 121 NRQAATAELRRSLAHFCTSLQGLLGSAGMATLGYPLPQPLPGTEPAWAPGAHSDFLQ 180
 Db 121 NRQAATAELRRSLAHFCTSLQGLLGSAGMATLGYPLPQPLPGTEPAWAPGAHSDFLQ 180
 QY 181 KMDDFWLLKELQTLWRSKADFNRLKKKQPPAASVTLHLEAHGF 225
 Db 181 KMDDFWLLKELQTLWRSKADFNRLKKKQPPAASVTLHLEAHGF 225

RESULT 2
 Q9UBD9 PRELIMINARY; PRT; 225 AA.
 AC Q9UBD9 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Neurotrophin-1/B-cell stimulating factor-3 (Cardiotrophin-like cytokine) (Similar to cardiotrophin-like cytokine, neurotrophin-1/B-cell stimulating factor-3).
 GN CUC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99432254; PubMed=10500198;
 RA Senaldi G., Varnum B.C., Samiento U., Starnes C., Lile J., Scully S., Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Manu F., Simonet W.S., Boone T., Chang M.-S.;
 RT "Novel neurotrophin-1/B cell-stimulating factor-3: A cytokine of the IL-6 family";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463 (1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=99382254; PubMed=10448081;
 RA Shi Y., Wang W., Yourey P.A., Gohari S., Zukauskas D., Zhang J., Ruben S., Alderson R.F.;
 RT "Computational EST database analysis identifies a novel member of the neurotrophic cytokine family";
 RL Biochem. Biophys. Res. Commun. 262:132-138 (1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Hu X., Xu Y., Zhang B., Peng X., Yuan J., Qiang B.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]

RP TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF176912; AAF00992.1; -
 DR EMBL; AF172854; AAD54284.1; -
 DR EMBL; AF176911; AAF00991.1; -
 DR EMBL; AY049779; AAL15436.1; -
 DR EMBL; BC012939; AAL12939.1; -
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0005125; F:cytokine activity; NAS.
 DR GO; GO:0019221; P:cytokine and chemokine mediated signaling p. .; NAS.
 SQ SEQUENCE 225 AA; 25176 MW; E2DD4B6280833B55 CRC64;

Query Match 97.5%; Score 1193; DB 4; Length 225;
 Best Local Similarity 96.3%; Pred. No. 1.8e-105; Indels 0; Gaps 0;
 Matches 219; Conservative 3; Mismatches 4;
 QY 1 MDRAGDSWGMACLTVMHLPAVPAALNRTGDPGPGSIQKTYDLTRYLHQLSLAGT 60
 Db 1 MDRAGDSWGMACLTVMHLPAVPAALNRTGDPGPGSIQKTYDLTRYLHQLSLAGT 60
 QY 61 YLNYLGPPNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTQNYEAYSHLLCYLRGL 120

Db 61 YLNYLGPPNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTQNYEAYSHLLCYLRGL 120
 QY 121 NRQAATAELRRSLAHFCTSLQGLLGSAGMATLGYPLPQPLPGTEPAWAPGAHSDFLQ 180
 Db 121 NRQAATAELRRSLAHFCTSLQGLLGSAGMATLGYPLPQPLPGTEPAWAPGAHSDFLQ 180
 QY 181 KMDDFWLLKELQTLWRSKADFNRLKKKQPPAASVTLHLEAHGF 225
 Db 181 KMDDFWLLKELQTLWRSKADFNRLKKKQPPAASVTLHLEAHGF 225

RESULT 3
 Q9PUJ1 PRELIMINARY; PRT; 215 AA.
 AC Q9PUJ1 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Receptivity factor isoform 2 precursor.
 GN PRF.
 OS Plethodon jordani (Jordan's salamander).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
 OC Plethodon.
 OC NCBI_TaxID=8336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99420364; PubMed=10489368;
 RA Rollmann S.M., Houck L.D., Feldhoff R.C.;
 RT "Proteinaceous pheromone affecting female receptivity in a terrestrial salamander";
 RL Science 285:1907-1909 (1999).
 DR EMBL; AF181481; AAF01026.1; -
 KW Signal.
 FT SIGNAL 1 23 POTENTIAL.
 SQ SEQUENCE 215 AA; 24080 MW; B341B8B7B4E28438 CRC64;

Query Match 11.8%; Score 144.5; DB 13; Length 215;
 Best Local Similarity 25.6%; Pred. No. 1.1e-05; Indels 7; Gaps 3;
 Matches 41; Conservative 31; Mismatches 81;
 QY 56 SLACTYLYLGGPPNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTQNYEAYSHLLC 115
 Db 55 SLPTLYLSPQAGPLSDPDYQLPHKIVANLFTAAVDYTFMKQDTETLNNLYFYSAIVE 114
 QY 116 YLR-GLNRQ----AATAELRRSLAHFCTSLQGLLGSAGMATLGYPLPQPLPGTEPAWA 170
 Db 115 FLKEAMTEQEDLNPAELSLKAKFEAMANSNTLISKISDINTQGMSTITLP--KPLVV 172
 QY 171 PGPAHSDFLQKMDDFWLLKELQTLWRSKADFNRLKKKQ 210
 Db 173 PFEGSAVFRKLRGCVCKYKERVLLTKEDFFFLAKYQ 212

RESULT 4
 Q9PUJ0 PRELIMINARY; PRT; 215 AA.
 AC Q9PUJ0 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Receptivity factor isoform 3 precursor.
 GN PRF.
 OS Plethodon jordani (Jordan's salamander).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
 OC Plethodon.
 OC NCBI_TaxID=8336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99420364; PubMed=10489368;
 RA Rollmann S.M., Houck L.D., Feldhoff R.C.;
 RT "Proteinaceous pheromone affecting female receptivity in a terrestrial

[illegible]

Db 182 LEIREGDPAALELAELAATLPLMPC-----DISKAERYRLLDASSYSL-- 228
QY 61 YLNYLGPPEPDEFPPRIGASTLPRATVNLVWRSNDRLRLTQNYEAYSH----- 112
Db 229 -----LPAFTNATPTDDAYSALAWHLGSSQRLAQYFNGHWRLQDQW 275
QY 113 -LLCYLRGLNRQAATAELRSLAHFCTSLQGLLSIAGVMATLVPLQPLPGTEPAWAP 171
Db 276 EMLGEALRTSLGQAAPTSTAQRLTALDALLE-----WRPLVQ--AQQEDADVR 325
QY 172 GPAHSDFLQMDPF-WLLKELQTLWRSKDF 202
Db 326 GAAHEQFLEELQDTRMGESFSLTSRLLARSW 357

RESULT 8
Q8N358 PRELIMINARY; PRT; 287 AA.
AC Q8N358;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Blood;
RC Strausberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028076; AAH28076.1; -
KW Hypothetical protein.
SQ SEQUENCE 287 AA; 32156 MW; 6E57LECA0328E74E CRC64;

Query Match 7.7%; Score 94; DB 4; Length 287;
Best Local Similarity 22.3%; Pred. No. 1.1;
Matches 47; Conservative 18; Mismatches 62; Indels 84; Gaps 9;

QY 15 LCTVLMHLPVAPALRTGDPGPGSIQKTYD-----LTRY---LEHQL--RSLAG 59
Db 132 LLPLVWLRP-----PDGPTLNLTLQCPGSRQSPGVLRFNQHLVLTGRAFTN 181
QY 60 TYLNY-----LGPPNEPDEFPPRIGASTLPRATVNLVWRSNDRLRLTQNYEAYSHL 115
Db 182 TYLFYGYRVGP-----ESSVYSIRLA 204
QY 116 YLRGLNRQAATAELRSLAHFCTSLQGLLSIA-----GVMATLVPLQPLPGTEPAW 169
Db 205 YL-----LSPLACLLLCFCGTLHOLLSTLASGPGGWPAPAHWPACPLPLGLPR 256
QY 170 APGPAHSDFLQK-----DDFWLLKELQTLW 196
Db 257 LPPPHQAQVLRAGAGMGDTWRGRSFLPWGW 287

RESULT 9
Q8GM87 PRELIMINARY; PRT; 8601 AA.
AC Q8GM87;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 25, Last annotation update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mixed type I polyketide synthase/nonribosomal peptide synthetase.
GN PEDF.
OS symbiont bacterium of Paederus fuscipes.
OC Bacteria.
OX NCBI_TaxID=176282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22294974; PubMed=12381784;
RA Piel J.;

RT "A polyketide synthase-peptide synthetase gene cluster from an
unclutured bacterial symbiont of Paederus bestles.",
Proc. Natl. Acad. Sci. U.S.A. 99:14002-14007(2002).
EMBL; AY059471; AAL27851.1; -
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0004459; F:l-lactate dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006096; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:glycolysis; IEA.
DR GO; GO:0009401; P:phenolpyruvate-dependent sugar phospho. . .; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002328; ADH_zinc.
DR InterPro; IPR000873; AMP_bind.
DR InterPro; IPR001242; Condensatn.
DR InterPro; IPR002114; Hpr SerP S.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR001557; L_LDH.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR006162; Phantne_S.
DR InterPro; IPR006163; Pp_bind.
DR InterPro; IPR000051; SAM_bind.
DR InterPro; IPR002155; Thiolase.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00501; AMP-binding; 1.
DR Pfam; PF00668; Condensation; 1.
DR Pfam; PF00109; ketoacyl-synt; 6.
DR Pfam; PF02801; ketoacyl-synt_C; 6.
DR Pfam; PF00550; pp-binding; 6.
DR PROSITE; PS00075; ACR_DOMAIN; 6.
DR PROSITE; PS00059; ADH_ZINC; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 3.
DR PROSITE; PS00064; L_LDH; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 2.
DR PROSITE; PS00589; PTS_HPR_SER; 1.
DR PROSITE; PS00098; THIOALASE_1; 1.
SQ SEQUENCE 8601 AA; 948046 MW; C498AC8B0B6082C7 CRC64;

Query Match 7.7%; Score 94; DB 2; Length 8601;
Best Local Similarity 26.1%; Pred. No. 88;
Matches 52; Conservative 33; Mismatches 72; Indels 42; Gaps 11;

QY 58 AGTYNLVILGPPPEPDEFPPRIGASTLPRATVNLVWRSNDRLRLTQNYEAYSHL 117
Db 5078 SGTNVHLVVEEFVRSNSDPRLDDVSSTAQPEL-ILLSTKDAERLS---EVLNLAHFV 5133
QY 118 RGLNRQAATAELRSLAHFCTSLQ-----LLGSTAGVWATL----- 154
Db 5134 RQAQNQPADLE-RLSLADLAYTLQTGREAMEQRVALLVGLDGLLEALSALREPRCPVS 5192
QY 155 ---GVPLPQPLPGTEPAWAPGPAHSDFLQKMDDFWL-----LKEI-QTWLRSKDFNRLK 206
Db 5193 VMSGRVEPGSRGAEVTNADQPA-AEILLQRIQP-WLAEGALDELAQAWAGAPIDWCQLR 5250
QY 207 KMQPPAASVTLLHLEAHGF 225
Db 5251 RR-RPPR---RVHLPSVPF 5265

RESULT 10
O54153 PRELIMINARY; PRT; 640 AA.
ID O54153;
AC O54153;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transferrase.
GN SC05890 OR SC3P7.10.
OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Oliver K., Harris D.;
 RA Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Parkhill J., Barrell B.G., Rastandream M.A.;
 RA Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RA "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RA "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RA "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RA "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RA "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RA "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RA "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
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 RL Mol. Microbiol. 21:77-96(1996).
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 RA Kinashi H., Hopwood D.A.;
 RA "A set of ordered cosmids and a detailed genetic and physical map for
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 RL Mol. Microbiol. 21:77-96(1996).
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 RL Mol. Microbiol. 21:77-96(1996).
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 RL Mol. Microbiol. 21:77-96(1996).
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 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
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RP SEQUENCE FROM N.A.
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 RA Kinashi H., Hopwood D.A.;
 RA "A set of ordered cosmids and a detailed genetic and physical map for
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 RL Mol. Microbiol. 21:77-96(1996).
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 RA Kinashi H., Hopwood D.A.;
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 RL Mol. Microbiol. 21:77-96(1996).
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 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
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 RL Mol. Microbiol. 21:77-96(1996).
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 RL Mol. Microbiol. 21:77-96(1996).
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 RA Kinashi H., Hopwood D.A.;
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 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
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 RA Kinashi H., Hopwood D.A.;
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 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
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 RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RA "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]

088841

ID 088841 PRELIMINARY; PRT; 727 AA.

AC 088841;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Faciogenital dysplasia protein 2.

GN FGD2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=99389726; PubMed=10458911;

RA Pasteris N.G., Gorski J.L.;

RA "Isolation, characterization, and mapping of the mouse and human fgd2

genes, faciogenital dysplasia (FGD1; aarskog syndrome) gene

homologues.";

RL Genomics 60:57-66(1999).

CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.

DR EMBL; AF017368; AAC35430.1; -.

DR MGD; MGI:1347084; Fgd2.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR InterPro; IPR001849; PH

DR InterPro; IPR000219; RhogEF.

DR Pfam; PF01363; FYVE; 1.

DR Pfam; PF00169; PH; 1.

DR Pfam; PF00621; RhogEF; 1.

DR SMART; SMO0064; FYVE; 1.

DR SMART; SMO0233; PH; 1.

DR SMART; SMO0325; RhogEF; 1.

DR PROSITE; PS00010; DH_2; 1.

DR PROSITE; PS00003; PH DOMAIN; 1.

DR PROSITE; PS0178; ZF FYVE; 1.

SQ SEQUENCE 727 AA; 82099 MW; 5CD0FBFB905C5FC5 CRC64;

Query Match

Best Local Similarity 7.6%; Score 93; DB 11; Length 727;

Matches 61; Conservative 32; Mismatches 93; Indels 60; Gaps 11;

Qy 21 HLPVAPALNRTGDPGPGSIQKTYDILTRYLEHQL-----RSLAGT 60

Db 13 NLVAVFENNRT--PGEAPGSHSLEDQPHIPEQLSLSPFWPEAPPVKEALKSEFRPVSKT 70

Qy 61 YLNYLGPPFN-----EPDNPPPLGAETLPRTVNLVWRSNDRRLRLTONYAYSH 112

Db 71 YLSSLNKLSSGAWRRSCQGVSP---GPE-----TQPEEXRVVRELLETEQAYVARLH 122

Qy 113 LL--CYLRGLNRQAATAELRRSLAHFCTSLQGLGSIAGVMA-TLGYPLPQPLPGTEPAW 169

Db 123 LLDQVFFQLLEAG-----RSKAPFEDVVKLIFPSNISSYIFRHAQFFLPE-LQRVDDW 176

Qy 170 AFGAHSDFLQKMDDFWLL-----KELQTLWRSKADFNRLKKKQPPPAASYT 217

Db 177 AATPRIGDVIOKLAPFLKNVSEYVKNFAERAEILLATMDKS-QPFQEVVTRIQCSEASS 235

Qy 218 LHLEAH 223

Db 236 LTLQHH 241

RESULT 12

Q8VBB1

ID Q8VBB1 PRELIMINARY; PRT; 200 AA.

AC Q8VBB1;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein BMEII0989.

GN BMEII0989.

OS Brucella melitensis.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN=16M / ATCC 23456 / Biotype 1;
 RC MEDLINE=20020109; PubMed=11756688;
 RX delvecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
 RA Seikov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrpides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
 DR EMBL; AB009732; AAL54231.1; ..
 DR PIR; AD3633; AD3633.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR InterPro; IPR008262; Lipase AS.
 DR PROSITE; PS00120; LIPASE SER; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 200 AA; 21513 MW; B4A8596707B67617 CRC64;
 Query Match 7.6%; Score 92.5; DB 16; Length 200;
 Best Local Similarity 23.9%; Pred. No. 0.93; Indels 65; Gaps 11;
 Matches 55; Conservative 21; Mismatches 89; Indels 65; Gaps 11;
 QY 10 GMLACLCTVLMHLPVAPALNRGTGDPGPGPSIQKTYDLTRYLHQLRSLAGTYLYNLGPPF 69
 Db 2 GLLAGALV---LPSLPAEAKTQAAMPNATSPHQADVYL---LRGFADIFSTGI--- 51
 QY 70 NEPDFNPPRLGAETLPATVNLV-----WRLNDRRLTQNYEAYSHLLCYLRLGNRQA 124
 Db 52 -----DEIGAE-LQAAGVNAHVQGHAAWRLNLRIVADQKNGHLFPVVLIGHSLGANA 103
 QY 125 A---TAEIRSLAHFCTSLQGLLSIAGVMTLGYPLPQPLPGT-----EPAW-- 169
 Db 104 AIVIAELER-----GIAVDYMTAATGPDPLPGNVRRVNVNFKQHGWL 151
 QY 170 --APGPAHSDFLQKDDFWLLKELQTLWRSKDFNRLK-KMQPPAAV 216
 Db 152 PLVGPGRFHGHLENRD-----FSNAKDVGHFNIKQRPLOAEV 189
 RESULT 13
 ID Q8FX31 PRELIMINARY; PRT; 232 AA.
 AC Q8FX31;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN BRA0258.
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29461;
 RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN=1330 / Biovar 1;
 RC MEDLINE=22247741; PubMed=12271122;
 RX Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Unayam L., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J., Van Aken S.B.,
 RA Riedmuller S., Petelin H., Gill S.R., White O., Salzberg S.L.,
 RA Hoover D.B., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
 DR EMBL; AE014526; AAN33460.1; ..
 DR TIGR; BRA0258; ..
 GO; GO:0003824; F:catalytic activity; IEA.

DR InterPro; IPR008262; Lipase AS.
 DR PROSITE; PS00120; LIPASE SER; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 232 AA; 24810 MW; 612CB963D7A56B18 CRC64;
 Query Match 7.6%; Score 92.5; DB 16; Length 232;
 Best Local Similarity 23.9%; Pred. No. 1.1; Indels 65; Gaps 11;
 Matches 55; Conservative 21; Mismatches 89; Indels 65; Gaps 11;
 QY 10 GMLACLCTVLMHLPVAPALNRGTGDPGPGPSIQKTYDLTRYLHQLRSLAGTYLYNLGPPF 69
 Db 34 GLLAGALV---LPSLPAEAKTQAAMPNATSPHQADVYL---LRGFADIFSTGI--- 83
 QY 70 NEPDFNPPRLGAETLPATVNLV-----WRLNDRRLTQNYEAYSHLLCYLRLGNRQA 124
 Db 84 -----DEIGAE-LQAAGVNAHVQGHAAWRLNLRIVADQKNGHLFPVVLIGHSLGANA 135
 QY 125 A---TAEIRSLAHFCTSLQGLLSIAGVMTLGYPLPQPLPGT-----EPAW-- 169
 Db 136 AIVIAELER-----GIAVDYMTAATGPDPLPGNVRRVNVNFKQHGWL 183
 QY 170 --APGPAHSDFLQKDDFWLLKELQTLWRSKDFNRLK-KMQPPAAV 216
 Db 184 PLVGPGRFHGHLENRD-----FSNAKDVGHFNIKQRPLOAEV 221
 RESULT 14
 Q8NEV9 PRELIMINARY; PRT; 243 AA.
 ID Q8NEV9;
 AC Q8NEV9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE IL-27 p28 subunit.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 SEQUENCE FROM N.A.
 RP Pfanz S., Timans J., Cheung J., Rosales R., Kanzler H., Gilbert J.,
 RA Hibbert L., Churakova T., Travis M., Vaisberg E., Blumenschein W.,
 RA Mattson J., Wagner J., To W., Zurawski S., McClanahan T., Gorman D.,
 RA Bazan F., de Waal Malefyt R., Rennick D., Kastelein R.;
 RT "IL-27 p28 subunit sequences";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY099296; AAM34498.1; ..
 DR Genbank; HGNC:19157; IL30.
 DR GO; GO:0005615; C:extracellular space; ISS.
 DR GO; GO:0045523; F:interleukin-27 receptor binding; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0005102; P:receptor binding; ISS.
 DR GO; GO:0045078; P:positive regulation of interferon-gamma bio. .; IDA.
 DR GO; GO:0042129; P:regulation of T-cell proliferation; ISS.
 DR GO; GO:0045625; P:regulation of T-helper 1 cell differentiation; IDA.
 SQ SEQUENCE 243 AA; 27476 MW; 2FA8A8E86CF61AE8 CRC64;
 Query Match 7.6%; Score 92.5; DB 4; Length 243;
 Best Local Similarity 23.3%; Pred. No. 1.2;
 Matches 57; Conservative 26; Mismatches 105; Indels 57; Gaps 9;
 QY 1 MDLRAGD-SWGMCLACLCTVL-----WHLPAVALNRGTGDPGPGPSIQK-----TYDL 46
 Db 1 MQGTAGDUGWRLSLLLPLLLVQGVGFPPPG-----RPQLSLQLRREFTVSLHL 53
 QY 47 TRYLEHQURSLAGTYLN-----YLGPPNEDFPNPRIGATLPATVNLVWRSLN 98
 Db 54 ARKLLSEVRGQAHFAEHLPGVNLVLLP-----LG-BQLPDVSLTFQAWRLS 101
 QY 99 DELRLTQNYEAYSHLLCYLRLGNRQAATAELRR-SLAHFCTSLQGLLSIAGVMTLGYPL 157
 Db 102 DPERLCFISTTLPQPHAPGLGLGTQGRWTNMRNQLWMLRLDLRLQHLRFQVLAAGFN 161

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158 1EQP-----LFGTEPANAGPSAHSDFLQKMDDFWLKBLQTLWRSKDF 202
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
162 LEEETEEEEERKGLPGALQSGAQVSWPQLSTYRLHLSLVLRAVRL 221
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
203 NRLKK 207
      |||:|||||:|||||:|||||:|||||:|||||:
222 LLLSK 226
      |||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 15

082G16	PRELIMINARY;	PRT;	860 AA.
ID	Q82G16		
AC	Q82G16;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Hypothetical protein.		
DE			
GN	SAV3911.		
OS	Streptomyces avermitilis.		
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;		
OC	Streptomycineae; Streptomycetaceae; Streptomyces.		
OX	NCBI_TaxID=33903;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;		
RC	MEDLINE=21477403; PubMed=11572948;		
RA	Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,		
RA	Kimura S., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.		
RA	Chinese M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.		
RA	Shinohara H., Shiba T., Sakaki Y., Hattori M.,		
RT	"Genome sequence of an industrial microorganism Streptomyces		
RT	avermitilis: deducing the ability of producing secondary		
RT	metabolites."		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).		
RL	[2]		

RP SEQUENCE FROM N.A.
 RX STRAIN=MA-4690 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RC MEDLINE=22608306; PubMed=12592562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism *Streptomyces avermectilis*.";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL: AP005037; BAC71623.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 860 AA; 9016 MW; C7F0123F70246BC5 CRC64;

Query Match	7.6%	Score 92.5;	DB 16;	Length 860;
Best Local Similarity	27.2%;	Pred. No. 6.2;		
Matches 56;	Conservative 22;	Mismatches 101;	Indels 27;	Gaps 9;

QY	5	AGDSKGMIACTCYL--WHLPVPAALNRTPDG-----PPFSIQTKYDLTRY	49
Db	288	AGQAYTALATVEELKDWH--EGGPVILRAGGLSVRLKRTAVALDVPETPAFWELT-Y	345
QY	50	LEHOLRSIAGTYNLYGPPNEPEDFPPLRGAETLPRATVNLVWRSNDRILRLTQV	109
Db	346	AAGLLADGGEABERYAATPAYDEWLELP--AAERWSRLAT--AWLAATRAGLVGG	400
QY	110	YSHLLCYL--RLGNRQAATASLRSLAHFCTSLGGLSGIAGVWATLGYPLQPLPG	168
Db	401	KERTLSALGPGGLDRSASEYRRVALLADLPGASAAPASVIALRW--ERPLGTHPS	458
QY	169	WAP--GPAHSDFLOKMDDFWLKELQ	192
Db	459	FPSSAPSSDDTLRLAENTLSEAE	484

Search completed: August 10, 2004, 06:47:49
Job time : 36 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2004, 06:43:28 ; Search time 48 Seconds
(without alignments)
1324.441 Million cell updates/sec

Title: US-09-931-704-5

Perfect score: 1224

Sequence: 1 MDLRAGDSWGMCLACTVLW.....KKKMQPPAASVTLLEAHGF 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1224	100.0	225	2	Aaw56142 Amino aci
2	1224	100.0	225	2	Aaw29716 Mouse neu
3	1224	100.0	225	3	Aay87814 Murine NN
4	1224	100.0	225	5	Aau78177 Mouse nov
5	1193	97.5	225	2	Aaw56141 Amino aci
6	1193	97.5	225	2	Aaw29715 Human neu
7	1193	97.5	225	2	Aaw94466 Human car
8	1193	97.5	225	3	Aay87813 Human NNT
9	1193	97.5	225	4	Ag63543 Amino aci
10	1193	97.5	225	5	Aau78176 Human nov
11	1193	97.5	253	4	Aam25831 Human pro
12	1181	96.5	223	4	Aae00828 Human car
13	1171	95.7	321	4	Abb11896 Human car
14	1171	95.7	321	4	Aam79399 Human pro
15	1167	95.3	215	3	Aab19587 Mouse int
16	1164	95.1	260	4	Aam78415 Human pro
17	1136	92.8	213	3	Aab19586 Human int
18	852	69.6	164	4	Aam20115 Peptide #
19	852	69.6	164	4	Abb40317 Peptide #
20	852	69.6	164	4	Aam34012 Peptide #
21	852	69.6	164	4	Abb24716 Protein #
22	852	69.6	164	4	Aam73827 Human bon
23	852	69.6	164	4	Aam61118 Human bra
24	852	69.6	164	4	Abg55577 Human liv
25	852	69.6	164	5	Abg43716 Human pep

26	156.5	12.8	208	2	AAV09197	Human DNA
27	154	12.6	208	2	AAV09196	Human DNA
28	110.5	9.0	203	2	AA83965	Mouse car
29	110.5	9.0	203	2	AA88204	Human car
30	110.5	9.0	203	2	AAW29237	Murine ca
31	110.5	9.0	203	7	ADC24999	Mouse CHF
32	109	8.9	471	6	ABU41629	Protein e
33	94	7.7	8601	6	AAO29660	Paederus
34	93	7.6	661	6	ABM67720	Phototrab
35	92.5	7.6	243	4	AAU08153	Human cyt
36	92.5	7.6	243	4	ABE20277	Human int
37	92.5	7.6	243	5	AGS32291	Human IL-
38	92.5	7.6	243	5	AAU76375	Human hel
39	92.5	7.6	243	6	ABU09749	Human var
40	92.5	7.6	243	6	ABG75877	Human cyt
41	92	7.5	332	3	AAG22132	Arabidops
42	92	7.5	332	3	AAG40321	Arabidops
43	91.5	7.5	201	2	AA83967	Human car
44	91.5	7.5	201	2	AAW29238	Human car
45	91.5	7.5	201	2	AAV06490	Human tum

ALIGNMENTS

RESULT 1

AAW56142
ID AAW56142 standard; protein; 225 AA.

XX AAW56142;
AC AC
DT 13-JUL-1998 (first entry)

DE Amino acid sequence of murine neurotrophic factor NNT-1.

XX Mouse; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
KW treatment; neurological disease; degeneration; Parkinson's disease;
KW amyotrophic lateral sclerosis; ALS; Alzheimers's disease; stroke.

OS Mus sp.

XX Key Location/Qualifiers
FT Peptide 1..27
FT Protein /note= "signal peptide"
FT Protein 28..225
FT Protein /note= "mature peptide"

XX US5741772-A.

XX 21-APR-1998.

XX 03-FEB-1997; 97US-00792019.

XX 03-FEB-1997; 97US-00792019.

XX (AMGB-) AMGEN INC.

XX Chang M;

XX WPI; 1998-260526/23.

XX N-PSDB; AAV22654.

XX Neurotrophic factor NNT-1 polypeptide and related nucleic acids - useful

XX for stimulating growth of motor and sympathetic neurons.

XX Claim 2; Fig 5; 4ipp; English.

XX The present sequence represents a murine neurotrophic factor, designated
CC NNT-1, which is capable of stimulating growth of motor or sympathetic
CC neurons. The NNT-1 protein is useful in the treatment of neurological
CC diseases characterised by the degeneration and death of particular
CC classes of neurons. These diseases specifically include Parkinson's
CC disease, amyotrophic lateral sclerosis (ALS), Alzheimers's disease, stroke

CC and various degenerative disorders affecting vision

XX Sequence 225 AA;

Query Match 100.0%; Score 1224; DB 2; Length 225;

Best Local Similarity 100.0%; Pred. NO. 1.3e-120;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSGMLACTCTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLHQLSLAGT 60
 DB 1 MDLRAGDSGMLACTCTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLHQLSLAGT 60
 QY 61 YLNYLGPFPNPPNPRGLGAETLPATVNLVWRSNDRLRLTONYAYSHLLCYLRL 120
 DB 61 YLNYLGPFPNPPNPRGLGAETLPATVNLVWRSNDRLRLTONYAYSHLLCYLRL 120
 QY 121 NRQATAEELRSLAHFCTSLQGLLSIAGVMTLGYPLPQPLGTEPAWAPGPAHSDFLQ 180
 DB 121 NRQATAEELRSLAHFCTSLQGLLSIAGVMTLGYPLPQPLGTEPAWAPGPAHSDFLQ 180

QY 181 KMDDFWLLKELOTWLRSAKDFNRLKKMQPPAASVTLHLEAHGF 225

DB 181 KMDDFWLLKELOTWLRSAKDFNRLKKMQPPAASVTLHLEAHGF 225

RESULT 2

AAW29716

ID AAW29716 standard; protein; 225 AA.

XX AC AAW29716;

XX DT 09-NOV-1998 (first entry)

XX DE Mouse neurotrophic factor NNT-1.

XX KW NNT-1; neurotrophic factor; mouse; antiinflammatory; adjuvant;

XX KW Alzheimer's disease; Parkinson's disease; Huntington's disease;

XX KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;

XX KW peripheral neuropathy; dystrophy; neural retina degeneration;

XX KW common variable immunodeficiency; CVID; selective IgA deficiency;

XX KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;

XX KW therapy.

XX OS Mus sp.

XX FH Key

XX FT Peptide

XX FT Protein

XX FT /label= Sig_peptide

XX FT /label= Mat_protein

XX PN W09833922-A1.

XX PD 06-AUG-1998.

XX PF 02-FEB-1998; 98WO-US002363.

XX PR 03-FEB-1997; 97US-00792019.

XX PR 30-JAN-1998; 98US-00016534.

XX PA (AMGE-) AMGEN INC.

XX PI Chang M, Elliot GS, Senaldi G, Sarmiento U;

XX DR WPI; 1998-437475/37.

XX DR N-PSDB; AAV47512.

XX PT Newly isolated nucleic acid encoding human or murine neurotrophic factor

XX PT NNT-1 - useful for treatment of neurological and immunological diseases

XX PT or inflammation, also as vaccine adjuvant.

XX PS Claim 13, Fig 5; 120pp; English.

XX

CC This is the amino acid sequence of a murine neurotrophic factor.
 CC designated NNT-1, that is a growth factor for neurons and for B or T
 CC cells. It was deduced from isolated NNT-1 cDNA (see AAV47512). Human NNT-
 CC 1 (see AAW29716) is also provided. Vectors and host cells for use in the
 CC production of human murine recombinant NNT-1 polypeptides. These are used
 CC to treat: (i) neurological or immunological diseases, specifically
 CC Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral
 CC sclerosis, Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy
 CC and degeneration of the neural retina or conditions characterised by T
 CC or B cell defects, e.g. common variable immunodeficiency (CVID),
 CC selective IgA deficiency, hypogammaglobulinaemia and X-linked
 CC agammaglobulinaemia (claimed), but many others disclosed; and (ii)
 CC inflammation. NNT-1 is also able to boost immunoreactivity and antibody
 CC production following vaccination, and, since it inhibits tumour necrosis
 CC factor production, it may also be useful for treating sepsis. In
 CC addition, cells that have been engineered to express NNT-1 can be
 CC implanted, or nucleic acids are delivered in gene therapy vectors
 XX Sequence 225 AA;

Query Match 100.0%; Score 1224; DB 2; Length 225;
 Best Local Similarity 100.0%; Pred. NO. 1.3e-120;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSGMLACTCTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLHQLSLAGT 60

DB 1 MDLRAGDSGMLACTCTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLHQLSLAGT 60

QY 61 YLNYLGPFPNPPNPRGLGAETLPATVNLVWRSNDRLRLTONYAYSHLLCYLRL 120

DB 61 YLNYLGPFPNPPNPRGLGAETLPATVNLVWRSNDRLRLTONYAYSHLLCYLRL 120

QY 121 NRQATAEELRSLAHFCTSLQGLLSIAGVMTLGYPLPQPLGTEPAWAPGPAHSDFLQ 180

DB 121 NRQATAEELRSLAHFCTSLQGLLSIAGVMTLGYPLPQPLGTEPAWAPGPAHSDFLQ 180

QY 181 KMDDFWLLKELOTWLRSAKDFNRLKKMQPPAASVTLHLEAHGF 225

DB 181 KMDDFWLLKELOTWLRSAKDFNRLKKMQPPAASVTLHLEAHGF 225

RESULT 3

AAW87814

ID AAW87814 standard; protein; 225 AA.

XX AC AAW87814;

XX DT 24-AUG-2000 (first entry)

XX DE Murine NNT-1 protein.

XX KW NNT-1; neurotrophic factor; nootropic; neuroprotective; treatment;

XX KW anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;

XX KW nervous system degeneration; Alzheimer's disease; Parkinson's disease;

XX KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; murine;

XX KW Huntington's disease; peripheral neuropathy; neural retina degeneration;

XX KW retinopathy; immune disorder; hematopoietic disorder.

XX OS Mus sp.

XX FN US6054294-A.

XX PD 25-APR-2000.

XX PF 12-DEC-1997; 97US-00988819.

XX PR 03-FEB-1997; 97US-00792019.

XX FA (AMGE-) AMGEN INC.

XX PI Chang M;

XX WPI; 2000-338492/29.

XX DR

DR N-PSDB; AAA39483.
XX New nucleic acids encoding neurotrophic factors useful for stimulating
PT growth of motor or sympathetic neurons for treating neuron cell damage.
XX
XX
PS Claim 2b; Fig 5; 42pp; English.
XX
XX This invention describes a novel nucleic acid molecule (I) encoding a
CC novel neurotrophic factor (NNT-1) (II) which has nootropic,
CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
CC ophthalmological activity. (I) is useful for producing NNT-1 polypeptides
CC which are useful for treating patients in whom various cells of the
CC central, autonomic, or peripheral nervous system have degenerated and/or
CC have been damaged by congenital disease, trauma, mechanical damage,
CC surgery, stroke, ischemia, infection, metabolic disease, nutritional
CC deficiency, malignancy and/or toxic agents. NNT-1 proteins are used to
CC treat diseases like Alzheimer's, Parkinson's, amyotrophic lateral
CC sclerosis, Charcot-Marie-Tooth syndrome, Huntington's disease, peripheral
CC neuropathy induced by diabetes or other metabolic disorders, and/or
CC dystrophies or degeneration of the neural retina such as retinitis
CC pigmentosa, drug-induced retinopathies, stationary forms of night
CC blindness, progressive cone-rod degeneration, immune disorders and
CC hematopoietic disorders. (I) is effective in treating neurological
CC conditions and promotes neuron regeneration. Neural functions are
CC effectively restored in patients suffering from various neurological
CC disorders. This sequence represents the murine NNT-1 protein described in
CC the method of the invention
XX
XX Sequence 225 AA;

Query Match 100.0%; Score 1224; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.3e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDLRAGDSWGMACLCCTVWLHPALNRTGDPGPGSIQKTYDLTRYLHQLRSIAGT 60
Db 1 MDLRAGDSWGMACLCCTVWLHPALNRTGDPGPGSIQKTYDLTRYLHQLRSIAGT 60
Qy 61 YLNYLGPPFPNPDNPPRLGAEITLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
Db 61 YLNYLGPPFPNPDNPPRLGAEITLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
Qy 121 NQQAATAEIRSLAHFCTSLQGLGSIAGVWATGYPLPQPLGTEPAWAGPAHSDFLQ 180
Db 121 NQQAATAEIRSLAHFCTSLQGLGSIAGVWATGYPLPQPLGTEPAWAGPAHSDFLQ 180
Qy 181 KMDDFWLLKELQTLWRSKADFNLKKMQPPAASVTLHLEAHGF 225
Db 181 KMDDFWLLKELQTLWRSKADFNLKKMQPPAASVTLHLEAHGF 225

RESULT 4
AAU78177
ID AAU78177 standard; protein; 225 AA.
XX AAU78177;
AC
XX
XX 05-JUN-2002 (first entry)
DT
XX
XX Mouse novel neurotrophic factor NNT1.
DE
XX
XX Mouse; NNT1; neurotrophic factor; IGE-related disease;
XX Type I allergic disease; allergic rhinitis; eczema; dermatitis;
XX pollinosis; asthma; immune disease; cancer; arteriosclerosis;
XX vascular restenosis; rheumatoid arthritis; psoriatic arthritis;
XX inflammatory arthritis; osteoarthritis; inflammatory joint disease;
XX autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
XX inflammatory bowel disease; transplant rejection; reproductive disorder;
XX graft versus host disease; infertility; miscarriage; preterm labour.
OS Mus sp.
XX
XX W0200215977-A2.
PN

XX 28-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-US025906.
XX PF
XX 18-AUG-2000; 2000US-0226436P.
XX PR 16-AUG-2001; 2001US-00931704.
XX (AMGE-) AMGEN INC.
PA
XX Senaldi G;
PI
XX WPI; 2002-280867/32.
DR N-PSDB; ABK11649.
DR
XX Treating Immunoglobulin E-related disease, modulating IGE levels in a
PT patient, preventing IGE-related disease and treating allergic diseases,
PT involves administering NNT-1 inhibitor to a patient.
XX
XX Claim 2; Fig 5; 63pp; English.
XX
XX The invention relates to treating Immunoglobulin E (IGE)-related disease,
CC modulating IGE levels in a patient, preventing an IGE-related disease,
CC and treating allergic diseases, comprising administering a
CC therapeutically effective amount of novel neurotrophic factor (NNT)-1
CC inhibitor to a patient. Also included are a method of diagnosing an IGE-
CC related disease or susceptibility to an IGE-related disease, by
CC determining the presence or amount of expression of an NNT1 polypeptide
CC encoded by a NNT1 nucleotide sequence, its fragment or naturally
CC occurring variant, and diagnosing an IGE-related disease or
CC susceptibility of an IGE-related disease based on the presence or amount
CC of expression of the polypeptide and a pharmaceutical composition for use
CC in treating IGE-related disease, comprising the NNT1 inhibitor. The NNT1
CC inhibitor is useful for preventing and treating IGE-related disease,
CC modulating IGE levels, and treating allergic diseases e.g. Type I
CC allergic disease, allergic rhinitis, eczema, dermatitis, pollinosis,
CC asthma, immune diseases and disorders, diseases involving abnormal cell
CC proliferation including cancer, arteriosclerosis and vascular restenosis,
CC diseases and conditions relating to dysfunction of immune system
CC including rheumatoid arthritis, psoriatic arthritis, inflammatory
CC arthritis, osteoarthritis, inflammatory joint disease, autoimmune
CC disease, multiple sclerosis, lupus, diabetes, inflammatory bowel disease,
CC transplant rejection, and graft versus host disease, and reproductive
CC diseases and disorders including infertility, miscarriage, preterm labour
CC and delivery, and endometriosis. The present sequence represents Mouse
CC NNT1
XX
XX Sequence 225 AA;

Query Match 100.0%; Score 1224; DB 5; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.3e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDLRAGDSWGMACLCCTVWLHPALNRTGDPGPGSIQKTYDLTRYLHQLRSIAGT 60
Db 1 MDLRAGDSWGMACLCCTVWLHPALNRTGDPGPGSIQKTYDLTRYLHQLRSIAGT 60
Qy 61 YLNYLGPPFPNPDNPPRLGAEITLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
Db 61 YLNYLGPPFPNPDNPPRLGAEITLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
Qy 121 NQQAATAEIRSLAHFCTSLQGLGSIAGVWATGYPLPQPLGTEPAWAGPAHSDFLQ 180
Db 121 NQQAATAEIRSLAHFCTSLQGLGSIAGVWATGYPLPQPLGTEPAWAGPAHSDFLQ 180
Qy 181 KMDDFWLLKELQTLWRSKADFNLKKMQPPAASVTLHLEAHGF 225
Db 181 KMDDFWLLKELQTLWRSKADFNLKKMQPPAASVTLHLEAHGF 225

RESULT 5
AAW56141
ID AAW56141 standard; protein; 225 AA.

XX AC AAW56141;
 XX DT 13-JUL-1998 (first entry)
 XX DE Amino acid sequence of human neurotrophic factor NNT-1.
 XX KW Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
 KW treatment; neurological disease; degeneration; Parkinson's disease;
 KW amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 FT Peptide 1..27
 FT Protein /note= "signal peptide"
 FT /note= "mature protein"
 XX US5741772-A.
 XX PD 21-APR-1998.
 XX PF 03-FEB-1997; 97US-00792019.
 XX PR 03-FEB-1997; 97US-00792019.
 XX PA (AMGE-) AMGEN INC.
 XX PI Chang M;
 XX WPI; 1998-260526/23.
 XX N-PSDB; AAV22652.
 XX Neurotrophic factor NNT-1 polypeptide and related nucleic acids - useful
 for stimulating growth of motor and sympathetic neurons.
 XX Claim 1; Fig 3; 4lpp; English.
 XX The present sequence represents a human neurotrophic factor, designated
 NNT-1, which is capable of stimulating growth of motor or sympathetic
 neurons. The NNT-1 protein is useful in the treatment of neurological
 diseases characterised by the degeneration and death of particular
 classes of neurons. These diseases specifically include Parkinson's
 disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, stroke
 and various degenerative disorders affecting vision
 XX Sequence 225 AA;
 Query Match 97.5%; Score 1193; DB 2; Length 225;
 Best Local Similarity 96.9%; Pred. No. 2.5e-117;
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDLRAGDSWGLACCTVWLHLPVAVPALNRTGDPGPGSIQKTYDLYLHQLRSLAGT 60
 DB 1 MDLRAGDSWGLACCTVWLHLPVAVPALNRTGDPGPGSIQKTYDLYLHQLRSLAGT 60
 QY 61 YLNYLGPPFPNPPRLGAETLPRTVNLVWRSNDRLRLTONYAYSHLLCYLRGL 120
 DB 61 YLNYLGPPFPNPPRLGAETLPRTVNLVWRSNDRLRLTONYAYSHLLCYLRGL 120
 QY 121 NRQATAEILRSIAHFCSTSQGLLSIAGVMTLGYPLPQPLPGTEPWAPGPAHSDFLQ 180
 DB 121 NRQATAEILRSIAHFCSTSQGLLSIAGVMTLGYPLPQPLPGTEPWAPGPAHSDFLQ 180
 QY 181 KMDDFWLLKELQTLWRSKDFNRLKKQKQPPAASVTLHLEAHGF 225
 DB 181 KMDDFWLLKELQTLWRSKDFNRLKKQKQPPAASVTLHLEAHGF 225
 RESULT 6
 AAW29715
 ID AAW29715 standard; protein; 225 AA.

XX AC AAW29715;
 XX DT 09-NOV-1998 (first entry)
 XX DE Human neurotrophic factor NNT-1.
 XX KW NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
 KW peripheral neuropathy; dystrophy; neural retina degeneration;
 KW common variable immunodeficiency; CVID; selective IGA deficiency;
 KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
 KW therapy.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 FT Peptide 1..27
 FT Protein /label= Sig_peptide
 FT /label= Mat_protein
 XX WO9833922-A1.
 XX PD 06-AUG-1998.
 XX PF 02-FEB-1998; 98WO-US002363.
 XX PR 03-FEB-1997; 97US-00792019.
 XX 30-JAN-1998; 98US-00016534.
 XX PA (AMGE-) AMGEN INC.
 XX PI Chang M, Elliot GS, Senaldi G, Sarmiento U;
 XX WPI; 1998-437475/37.
 XX N-PSDB; AAV47510, AAV47511.
 XX Newly isolated nucleic acid encoding human or murine neurotrophic factor
 NNT-1 - useful for treatment of neurological and immunological diseases
 or inflammation, also as vaccine adjuvant.
 XX Claim 12; Fig 3; 120pp; English.
 XX This is the amino acid sequence of a novel neurotrophic factor,
 designated NNT-1, that is a growth factor for neurons and for B or T
 cells. It was deduced from isolated cDNA (see AAV47510) and genomic DNA
 (see AAV47511) clones. Vectors containing the cDNA or genomic DNA and
 host cells are provided for use in the production of NNT-1 polypeptides.
 These are used to treat: (i) neurological or immunological diseases,
 specifically Alzheimer's, Parkinson's or Huntington's diseases,
 amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, peripheral
 neuropathy, dystrophy and degeneration of the neural retina, or
 conditions characterised by T or B cell defects, e.g. common variable
 immunodeficiency (CVID), selective IGA deficiency, hypogammaglobulinaemia
 and X-linked agammaglobulinaemia (claimed), but many others disclosed;
 and (ii) inflammation. NNT-1 is also able to boost immunoreactivity and
 antibody production following vaccination, and, since it inhibits tumour
 necrosis factor production, it may also be useful for treating sepsis. In
 addition, cells that have been engineered to express NNT-1 can be
 CC implanted, or nucleic acids are delivered in gene therapy vectors
 XX Sequence 225 AA;
 Query Match 97.5%; Score 1193; DB 2; Length 225;
 Best Local Similarity 96.9%; Pred. No. 2.5e-117;
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDLRAGDSWGLACCTVWLHLPVAVPALNRTGDPGPGSIQKTYDLYLHQLRSLAGT 60
 DB 1 MDLRAGDSWGLACCTVWLHLPVAVPALNRTGDPGPGSIQKTYDLYLHQLRSLAGT 60

CC treat diseases like Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
 CC sclerosis, Charcot-Marie-Tooth syndrome, Huntington's disease, peripheral
 CC neuropathy induced by diabetes or other metabolic disorders, and/or
 CC dystrophies or degeneration of the neural retina such as retinitis
 CC pigmentosa, drug-induced retinopathies, stationary forms of night
 CC blindness, progressive cone-rod degeneration, immune disorders and
 CC hematopoietic disorders. (II) is effective in treating neurological
 CC conditions and promotes neuron regeneration. Neural functions are
 CC effectively restored in patients suffering from various neurological
 CC disorders. This sequence represents the human NNT-1 protein described in
 CC the method of the invention
 XX
 SQ Sequence 225 AA;

Query Match 97.5%; Score 1193; DB 3; Length 225;
 Best Local Similarity 96.9%; Pred. No. 2.5e-117;
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDLRAGDSWGMGLACTVWLHLPVAVPALNRTGDPGPGSIQKTYDTRYLEHQLRSLAGT 60
 DB 1 MDLRAGDSWGMGLACTVWLHLPVAVPALNRTGDPGPGSIQKTYDTRYLEHQLRSLAGT 60
 QY 61 YLNYLGPPFPNEPDPNPPRLGAETLPRATVNVLRSLNDRRLKLTQNYEAYSHLLCYLRGL 120
 DB 61 YLNYLGPPFPNEPDPNPPRLGAETLPRATVNVLRSLNDRRLKLTQNYEAYSHLLCYLRGL 120
 QY 121 NRQAATAELRRSLAHFCTSLQGLLGSAGVMATLGYPLPQPLGTEPAWAPGPAHSDFLQ 180
 DB 121 NRQAATAELRRSLAHFCTSLQGLLGSAGVMATLGYPLPQPLGTEPAWAPGPAHSDFLQ 180
 QY 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMQPPAAVTLHLEAHGF 225
 DB 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMQPPAAVTLHLEAHGF 225

RESULT 9
 AAG63543
 ID AAG63543 standard; protein; 225 AA.
 XX AC AAG63543;
 XX DT 15-OCT-2001 (first entry)
 XX DE Amino acid sequence of a human NNT-1 protein.
 XX KW NNT-1; CLF-1; sCNTFRalpha; nervous system; neuron; nervous system;
 KW neuro-muscular function; tumour; immune system; haematopoietic system;
 KW reproductive system; liver; skeletal muscle; neurodegenerative disease;
 KW amyotrophic lateral sclerosis; Parkinson's disease; Huntington's disease;
 KW muscular mass; paralysis; cancer; obesity; fertility; endometriosis;
 KW blastocyst implantation; thrombosis; retinal disease;
 XX KW retinal pigmentosis.
 XX OS Homo sapiens.
 XX PN WO200155172-A2.
 XX PD 02-AUG-2001.
 XX PF 26-JAN-2001; 2001WO-FR000253.
 XX PR 27-JAN-2000; 2000PR-00001035.
 XX PR 12-OCT-2000; 2000PR-00013089.
 XX PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX PI Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gascan H;
 XX WPI; 2001-488773/53.
 XX DR N-PSDB; AAH74484.
 XX PA A complex comprising a NNT-1 protein and a CLF-1 and/or sCNTFRalpha

PT protein useful to treat neurodegenerative disease including Parkinson's
 PT and Huntington's, obesity and cancer.
 XX
 PS Claim 2; Page 58; 67pp; French.
 XX
 CC The present sequence represents a human NNT-1 protein. The specification
 CC describes a complex comprising a NNT-1 protein and a CLF-1 and/or
 CC sCNTFRalpha protein. The NNT-1/CLF-1 complex is used to modulate activity
 CC of the sCNTFRalpha/gp130/LIFbeta receptor complex, or to induce
 CC phosphorylation of the tyrosine of gp130 and LIFbeta, particularly where
 CC cells expressing the receptor complex are in the central or peripheral
 CC nervous system, in neurons implicated in neuro-muscular function or in
 CC skeletal muscle. The complex or antibodies are also used to decrease the
 CC survival, growth or proliferation of tumour cells or to facilitate the
 CC proliferation and/or inhibit differentiation of cells stocks. The complex
 CC is also used to modulate activity of the gp130/LIFbeta receptor or cells
 CC expressing that receptor, particularly those cells implicated in the
 CC immune, haematopoietic, nervous or reproductive system, the liver or
 CC skeletal muscle. Molecules of the invention may be used to prevent or
 CC treat neurodegenerative diseases including amyotrophic lateral sclerosis,
 CC Parkinson's and Huntington's disease, to repair or regenerate nervous or
 CC muscular tissue or to maintain muscular mass in paralysis patients. They
 CC may also be used to treat cancer, obesity and associated diseases, and to
 CC improve fertility, particularly to avoid endometriosis and/or assist
 CC blastocyst implantation, thrombosis, or retinal disease, particular
 CC retinal pigmentosis
 XX
 SQ Sequence 225 AA;

Query Match 97.5%; Score 1193; DB 4; Length 225;
 Best Local Similarity 96.9%; Pred. No. 2.5e-117;
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDLRAGDSWGMGLACTVWLHLPVAVPALNRTGDPGPGSIQKTYDTRYLEHQLRSLAGT 60
 DB 1 MDLRAGDSWGMGLACTVWLHLPVAVPALNRTGDPGPGSIQKTYDTRYLEHQLRSLAGT 60
 QY 61 YLNYLGPPFPNEPDPNPPRLGAETLPRATVNVLRSLNDRRLKLTQNYEAYSHLLCYLRGL 120
 DB 61 YLNYLGPPFPNEPDPNPPRLGAETLPRATVNVLRSLNDRRLKLTQNYEAYSHLLCYLRGL 120
 QY 121 NRQAATAELRRSLAHFCTSLQGLLGSAGVMATLGYPLPQPLGTEPAWAPGPAHSDFLQ 180
 DB 121 NRQAATAELRRSLAHFCTSLQGLLGSAGVMATLGYPLPQPLGTEPAWAPGPAHSDFLQ 180
 QY 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMQPPAAVTLHLEAHGF 225
 DB 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMQPPAAVTLHLEAHGF 225

RESULT 10
 AAU78176
 ID AAU78176 standard; protein; 225 AA.
 XX AC AAU78176;
 XX DT 05-JUN-2002 (first entry)
 XX DE Human novel neurotrophic factor NNT1.
 XX KW Human; NNT1; neurotrophic factor; IgE-related disease;
 KW Type I allergic disease; allergic rhinitis; eczema; dermatitis;
 KW pollinosis; asthma; immune disease; cancer; arteriosclerosis;
 KW vascular restenosis; rheumatoid arthritis; psoriatic arthritis;
 KW inflammatory arthritis; osteoarthritis; inflammatory joint disease;
 KW autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
 KW inflammatory bowel disease; transplant rejection; reproductive disorder;
 KW graft versus host disease; infertility; miscarriage; preterm labour.
 XX OS Homo sapiens.
 XX PN WO200215977-A2.

```

PD 28-FEB-2002.
XX
XX
XX PF 17-AUG-2001; 2001WO-US025906.
XX
XX PR 18-AUG-2000; 2000US-0226436P.
XX PR 16-AUG-2001; 2001US-00931704.
XX
XX PA (AMGE-) AMGEN INC.
XX
XX PI Senaldi G;
XX
XX WPI; 2002-280867/32.
XX DR N-PSDB; ABK11647.
XX
XX
XX PT Treating Immunoglobulin E-related disease, modulating IGE levels in a
XX PT patient, preventing IGE-related disease and treating allergic diseases,
XX PT involves administering NNT-1 inhibitor to a patient.
XX
XX PS Claim 2; Fig 3; 63pp; English.
XX
XX CC The invention relates to treating Immunoglobulin E (IGE)-related disease,
XX CC modulating IGE levels in a patient, preventing an IGE-related disease,
XX CC and treating allergic diseases, comprising administering a
XX CC therapeutically effective amount of novel neurotrophic factor (NNT)-1
XX CC inhibitor to a patient. Also included are a method of diagnosing an IGE-
XX CC related disease or susceptibility to an IGE-related disease, by
XX CC determining the presence or amount of expression of an NNT1 polypeptide
XX CC encoded by a NNT1 nucleotide sequence, its fragment or naturally
XX CC occurring variant, and diagnosing an IGE-related disease or
XX CC susceptibility of an IGE-related disease based on the presence or amount
XX CC of expression of the polypeptide and a pharmaceutical composition for use
XX CC in treating IGE-related disease, comprising the NNT1 inhibitor. The NNT1
XX CC inhibitor is useful for preventing and treating IGE-related disease,
XX CC modulating IGE levels, and treating allergic diseases e.g. Type 1
XX CC allergic disease, allergic rhinitis, eczema, dermatitis, pollinosis,
XX CC asthma, immune diseases and disorders, diseases involving abnormal cell
XX CC proliferation including cancer, arteriosclerosis and vascular restenosis,
XX CC diseases and conditions relating to dysfunction of immune system
XX CC including rheumatoid arthritis, psoriatic arthritis, inflammatory
XX CC arthritis, osteoarthritis, inflammatory joint disease, autoimmune
XX CC disease, multiple sclerosis, lupus, diabetes, inflammatory bowel disease,
XX CC transplant rejection, and graft versus host disease, and reproductive
XX CC diseases and disorders including infertility, miscarriage, preterm labour
XX CC and delivery, and endometriosis. The present sequence represents human
XX CC NNT1
XX
XX SQ Sequence 225 AA;
XX
XX Query Match 97.5%; Score 1193; DB 5; Length 225;
XX Best Local Similarity 96.9%; Pred. No. 2.5e-117;
XX Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 MDLRAGDSGMLACLCTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLHQLRSLAGT 60
DB 1 MDLRAGDSGMLACLCTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLHQLRSLAGT 60
XX
QY 61 YLNYLGPFPNEPDPRLGATTLPRATVNLWRSNDRLRLTONYAYSHLLCYLRGL 120
DB 61 YLNYLGPFPNEPDPRLGATTLPRATVNLWRSNDRLRLTONYAYSHLLCYLRGL 120
XX
QY 121 NRQATAELRRSLAHFTCSLQGLLSIAGVWATLGYPLPQPLGTPETAWAGPAAHSDPLQ 180
DB 121 NRQATAELRRSLAHFTCSLQGLLSIAGVWATLGYPLPQPLGTPETAWAGPAAHSDPLQ 180
XX
QY 181 KMDDFWLLKELQTLWRSKAFNRLKKMQPPAAASVTLHLEAHGF 225
DB 181 KMDDFWLLKELQTLWRSKAFNRLKKMQPPAAASVTLHLEAHGF 225
XX
XX RESULT 11
XX AAM25831
XX ID AAM25831 standard; protein; 253 AA.
XX

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AC AAM25831;
XX
XX DT 16-OCT-2001 (first entry)
XX
XX DE Human protein sequence SEQ ID NO:1346.
XX
XX KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
XX KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
XX KW antibacterial; endocrine; cardiant; central nervous system; virucide;
XX KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
XX KW antiagregant; haemostatic; vulnery; antitumor; osteopathic; eczema;
XX KW dermatological; antiallergic; antidiabetic; antidiabetic; cytostatic;
XX KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
XX KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
XX KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
XX KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
XX KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
XX KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
XX KW allergic rhinitis; diabetes; multiple sclerosis; depression; disorder;
XX KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
XX KW neurological disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO200153455-A2.
XX
XX PD 26-JUL-2001.
XX
XX PF 22-DEC-2000; 2000WO-US035017.
XX
XX PR 21-DEC-1999; 99US-00471275.
XX PR 21-JAN-2000; 2000US-0048725.
XX PR 23-APR-2000; 2000US-00552317.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-457603/49.
XX DR N-PSDB; AAH99772.
XX
XX FT Isolated human polynucleotides encoding polypeptides, useful for the
XX FT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
XX
XX PS Claim 20; Page 278; 1217pp; English.
XX
XX CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
XX CC AAM25863. The proteins can have activities based on the tissues and cells
XX CC they are expressed in, such as: antiinflammatory; antirheumatic;
XX CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
XX CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
XX CC cardiovascular; antianaemic; antiagregant; haemostatic; vulnery;
XX CC antitumor; osteopathic; dermatological; antiallergic; antidiabetic;
XX CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
XX CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
XX CC encoding them can be used in gene therapy, antisense therapy and vaccine
XX CC production. The proteins and polynucleotides are useful for screening for
XX CC agonists or antagonists of a protein and for the treatment and diagnosis
XX CC of disorders associated with the activity of a protein e.g. inflammation,
XX CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
XX CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
XX CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
XX CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
XX CC osteoporosis, severe combined immunodeficiency, eczema, allergic
XX CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
XX CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
XX CC neurological disorders
XX
XX SQ Sequence 253 AA;
XX
XX Query Match 97.5%; Score 1193; DB 4; Length 253;
XX Best Local Similarity 96.9%; Pred. No. 2.9e-117;
XX Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 MDLRAGDSWGLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGT 60
 DB 29 MDLRAGDSWGLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGT 88
 QY 61 YLYNLGPPFPNEPDPNPRGLGAETLPRATVNLVWRSNDRLRLTQNYEAYSHLLCYLRGL 120
 DB 89 YLYNLGPPFPNEPDPNPRGLGAETLPRATVNLVWRSNDRLRLTQNYEAYSHLLCYLRGL 148
 QY 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAITGYPPLPGTEPAPAWPGPAHSDFLQ 180
 DB 149 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAITGYPPLPGTEPAPAWPGPAHSDFLQ 208
 QY 181 KMDDFWLLKELQTLWRSKDFNRLKKMKQPPAAAVTLHLEAHG 225
 DB 209 KMDDFWLLKELQTLWRSKDFNRLKKMKQPPAAAVTLHLEAHG 253
 RESULT 12
 AAE00828
 ID AAE00828 standard; protein; 223 AA.
 AC AAE00828;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Human cardiotrophin-like cytokine (CLC) protein.
 XX
 KW Human; biologically active complex; haemopoietin receptor; NR6;
 KW cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
 KW differentiation; cell survival; neurotrophic activity.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..27
 FT /label= Signal_peptide
 FT Protein 28..223
 FT /label= Human_mature_CLC_protein
 FT /note= "Cardiotrophin-like cytokine"
 XX
 PN WO200127157-A1.
 XX
 PD 19-APR-2001.
 XX
 PF 06-OCT-2000; 2000WO-AU001216.
 XX
 PR 08-OCT-1999; 99AU-00003327.
 PR 12-MAY-2000; 2000AU-00007489.
 XX
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 PI Nash A, Jachno KM, Fabri LJ, Reid X, Bartlett PF, Hilton DJ;
 PI Nakata Y, Hasegawa M;
 XX
 DR WPI; 2001-281978/29.
 DR N-PSDB; AAD04201.
 XX
 PT New biologically active complex comprising NR6 and cardiotrophin-like-
 PT cytokine, for facilitating proliferation, differentiation and/or survival
 PT of a cell.
 XX
 PS Claim 32; Page 114-115; 123pp; English.
 XX
 CC The present invention relates to a biologically active complex comprising
 CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC). The
 CC complex is useful in the manufacture of a medicament for the treatment
 CC and/or prophylaxis of a subject, as it is involved in facilitating
 CC proliferation, differentiation and/or survival of a cell. The complex or
 CC its components have neurotrophic activity. The present sequence is human
 CC cardiotrophin-like cytokine (CLC) protein
 XX
 SQ Sequence 223 AA;

Query Match 96.5%; Score 1181; DB 4; Length 223;
 Best Local Similarity 96.9%; Pred. No. 4.5e-116;
 Matches -216; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDLRAGDSWGLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGT 60
 DB 1 MDLRAGDSWGLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGT 60
 QY 61 YLYNLGPPFPNEPDPNPRGLGAETLPRATVNLVWRSNDRLRLTQNYEAYSHLLCYLRGL 120
 DB 61 YLYNLGPPFPNEPDPNPRGLGAETLPRATVNLVWRSNDRLRLTQNYEAYSHLLCYLRGL 120
 QY 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAITGYPPLPGTEPAPAWPGPAHSDFLQ 180
 DB 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAITGYPPLPGTEPAPAWPGPAHSDFLQ 180
 QY 181 KMDDFWLLKELQTLWRSKDFNRLKKMKQPPAAAVTLHLEAH 223
 DB 181 KMDDFWLLKELQTLWRSKDFNRLKKMKQPPAAAVTLHLEAH 223
 RESULT 13
 ABB11896
 ID ABB11896 standard; peptide; 321 AA.
 AC ABB11896;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human cardiotrophin-like cytokine homologue, SEQ ID NO:2265.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; anti-inflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US003800.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-457740/49.
 DR N-PSDB; ABA09140.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 PS Claim 20; Page 273; 1963pp; English.
 XX
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a

CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention

Sequence 321 AA;

Query Match 95.7%; Score 1171; DB 4; Length 321;

Best Local Similarity 96.0%; Pred. No. 8.5e-115;

Matches 214; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 LRAGDSWGMACLCCTVWLHLPVAPALNRTGDPGPGPSIQKTYDLYLHQLRSLAGTYL 62
 Db 99 LPTGDSWGMACLCCTVWLHLPVAPALNRTGDPGPGPSIQKTYDLYLHQLRSLAGTYL 158
 QY 63 NYLGPPFNPDNPPRLGAETLPRAVNLVWRSNDRLRLTONYAYSHLLCYLRGLNR 122
 Db 159 NYLGPPFNPDNPPRLGAETLPRAVNLVWRSNDRLRLTONYAYSHLLCYLRGLNR 218
 QY 123 QAATAELRSLAHFCTSLQGLLSIAGVMAATLGYPLPQPLGTPAWAGPAHSDFLQKM 182
 Db 219 QAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLGTPAWAGPAHSDFLQKM 278
 QY 183 DDFWLLKELQTLWRSKDFNRLKKMKOPPAASVTLHLEAHGF 225
 Db 279 DDFWLLKELQTLWRSKDFNRLKKMKOPPAASVTLHLEAHGF 321

RESULT 14

AAW79399

ID AAW79399 standard; protein; 321 AA.

XX AC AAW79399;

XX DT 06-NOV-2001 (first entry)

XX DE Human protein SEQ ID NO 3045.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

OS Homo sapiens.
 XX WO200157190-A2.
 XX 09-AUG-2001.
 XX 05-FEB-2001; 2001WO-US004098.
 XX 03-FEB-2000; 2000US-00496914.
 XX 27-APR-2000; 2000US-00560875.
 XX 20-JUN-2000; 2000US-00598075.
 XX 19-JUL-2000; 2000US-00620325.
 XX 01-SEP-2000; 2000US-00654936.
 XX 15-SEP-2000; 2000US-00663561.
 XX 20-OCT-2000; 2000US-00693325.
 XX 30-NOV-2000; 2000US-00728422.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu Q, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 XX Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI; 2001-476283/51.
 XX N-PSDB; AAKS2532.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 XX in diagnosis and gene therapy.
 XX Claim 20; Page 237; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication

Sequence 321 AA;

Query Match 95.7%; Score 1171; DB 4; Length 321;

Best Local Similarity 96.0%; Pred. No. 8.5e-115;

Matches 214; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 LRAGDSWGMACLCCTVWLHLPVAPALNRTGDPGPGPSIQKTYDLYLHQLRSLAGTYL 62
 Db 99 LPTGDSWGMACLCCTVWLHLPVAPALNRTGDPGPGPSIQKTYDLYLHQLRSLAGTYL 158
 QY 63 NYLGPPFNPDNPPRLGAETLPRAVNLVWRSNDRLRLTONYAYSHLLCYLRGLNR 122
 Db 159 NYLGPPFNPDNPPRLGAETLPRAVNLVWRSNDRLRLTONYAYSHLLCYLRGLNR 218
 QY 123 QAATAELRSLAHFCTSLQGLLSIAGVMAATLGYPLPQPLGTPAWAGPAHSDFLQKM 182
 Db 219 QAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLGTPAWAGPAHSDFLQKM 278
 QY 183 DDFWLLKELQTLWRSKDFNRLKKMKOPPAASVTLHLEAHGF 225
 Db 279 DDFWLLKELQTLWRSKDFNRLKKMKOPPAASVTLHLEAHGF 321

RESULT 15

AAAB19587

ID AAB19587 standard; protein; 215 AA.

XX AC AAB19587;

Tue Aug 17 06:05:02 2004

us-09-931-704-5.rag

db 181 LOTWLWRS AKDFNRLKKMQPPAASVTLHLEAHGF 215

Search completed: August 10, 2004, 06:46:00
Job time : 49 secs

Job time : 49 secs

XX	22-JAN-2001 (first entry)
DT	
XX	
XX	Mouse interleukin-B60 (IL-B60).
DE	
XX	
XX	Interleukin-B60; IL-B60; mouse; cytokine-like factor-1;
KW	haematopoietic; inflammation; anti-inflammatory; autoimmune disease;
KW	therapy.
KW	

Accession	Protein	Location/Qualifiers
OS	Mus musculus.	
XX		
FH	Key	1..17
FT	Peptide	/label= signal_peptide
FT		18..215
FT	Protein	/label= Mature-protein
FT		

PN WO200053631-A1.

14-SEP-2000.

09-MAR-2000; 2000WO-US0006182.

XX
PR 11-MAR-1999: 99US-00267901.

XX
PA (SCHE) SCHEITNG CORP.

XX
PT
Oonnann B. Timans JC. Kastelein RA, Bazan JF;

XX
WPT: 2000-587426/55
DB

DR WPI; 2000-5875267
DR N-PSDB: AAA88547.

XX
PT Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
PT polypeptides, and nucleic acids, useful in research, diagnosis and for
XX treating inflammatory and autoimmune disorders.

xx
ps
Claim 1: Page 17: 97pp: English.

The present sequence is that of mouse interleukin-B60 (IL-B60), a novel, small soluble cytokine-like protein that exhibits structural motifs characteristic of a member of the long-chain cytokines, and which shows homology to granulocyte colony stimulating factor and interleukin-6. IL-60B may have either stimulatory or inhibitory effects on haematopoietic cells, including e.g. lymphoid cells, such as T-cells, B-cells, natural killer cells, macrophages, dendritic cells, haematopoietic progenitors, etc. Methods are provided for modulating the physiology or development of a cell or tissue culture cells by contacting the cell with an agonist or antagonist of IL-B60 or an agonist of antagonist of a complex of mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see AAB19588). The IL-B60/CLF-1 cytokine serves as a key physiological factor in motor neuron development and regeneration. IL-60B, its agonists and antagonists may be used to treat inflammatory or autoimmune disorders and also for drug screening.

Sequence 215 AA:

Query Match	95.3%	Score 1167	DB 3	Length 215
Best Local Similarity	100.0%	Pred. No. 1.3e-114		
Matches 215	Conservative	0	Mismatches 0	Gaps 0

11 M.A.C.T.VI.WHI.PAVPALNRTGDPGGPSIOKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70

1 MI.ACI.CTVI.WHI.PAVPAI.NRTGDPGPGPSIOKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60

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137 RSLAHFCTSLGSLGIAGVMATLGYPLPQPLPGTEPAWAPGPAHSDFLQKMDDFWLLKE 190

121 RSI AHETSLOGLLGSIAGVMATLGYPLPOPLPGTEPAWAPCPAHSDFLQKMDDFWLLKE 180

191 LOTWLRSAKDFNRLKKQMOPPAASVTILHLEAHGF 225

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 06:46:33 ; Search time 513 Seconds

(without alignments)
137.580 Million cell updates/sec

Title: US-09-931-704-5

Perfect score: 1224

Sequence: 1 MDLRAGDSWGMCLCTVLM.....KKXQPPAASVTLLEAHGF 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1224	100.0	225	9	US-09-931-704-5
2	1193	97.5	225	9	US-09-931-704-2
3	1193	97.5	225	14	US-10-212-793-2
4	1193	97.5	225	15	US-10-408-765A-795
5	1193	97.5	253	12	US-10-296-115-1346
6	1171	95.7	321	12	US-10-276-774-2266
7	852	69.6	164	9	US-09-864-761-40014
8	118.5	9.7	203	14	US-10-212-793-3
9	110.5	9.0	203	9	US-09-896-856-3
10	110.5	9.0	203	14	US-10-107-931-3
11	110.5	9.0	203	15	US-10-407-303-3
12	110.5	9.0	203	16	US-10-722-095-3
13	109	8.9	471	12	US-10-282-122A-69553
14	93	7.6	727	15	US-10-231-913-98
15	92.5	7.6	243	9	US-09-810-052-5

16	92.5	7.6	243	10	US-09-791-497-8	Sequence 8, Appli
17	92.5	7.6	243	13	US-10-000-776-6	Sequence 6, Appli
18	92.5	7.6	860	14	US-10-156-761-11445	Sequence 11445, A
19	91.5	7.5	201	9	US-09-901-540-3	Sequence 3, Appli
20	91.5	7.5	201	9	US-09-896-856-8	Sequence 8, Appli
21	91.5	7.5	201	9	US-09-901-257-3	Sequence 3, Appli
22	91.5	7.5	201	14	US-10-107-931-8	Sequence 8, Appli
23	91.5	7.5	201	14	US-10-212-793-4	Sequence 4, Appli
24	91.5	7.5	201	15	US-10-407-303-8	Sequence 8, Appli
25	91.5	7.5	201	16	US-10-722-095-8	Sequence 8, Appli
26	90	7.4	195	9	US-09-770-361-5	Sequence 5, Appli
27	90	7.4	195	14	US-10-226-759-5	Sequence 5, Appli
28	90	7.4	195	14	US-10-281-643-5	Sequence 5, Appli
29	90	7.4	195	15	US-10-383-916-5	Sequence 5, Appli
30	87	7.1	242	10	US-09-791-497-2	Sequence 2, Appli
31	87	7.1	242	13	US-10-000-776-2	Sequence 2, Appli
32	86.5	7.1	285	14	US-10-156-761-9399	Sequence 26, Appli
33	86.5	7.1	1022	12	US-10-188-186-26	Sequence 3, Appli
34	86.5	7.1	1429	12	US-10-029-347-3	Sequence 3, Appli
35	86.5	7.1	1429	14	US-10-028-374-3	Sequence 3, Appli
36	86.5	7.1	1429	14	US-10-183-770-3	Sequence 3, Appli
37	86	7.0	232	9	US-09-810-052-2	Sequence 2, Appli
38	86	7.0	1313	12	US-10-437-421-22	Sequence 22, Appli
39	85.5	7.0	389	15	US-10-369-493-22941	Sequence 22941, A
40	85.5	7.0	1122	16	US-10-437-963-141105	Sequence 141105, A
41	85	6.9	1009	12	US-10-433-802-11	Sequence 11, Appli
42	85	6.9	1009	16	US-10-332-947-47	Sequence 47, Appli
43	84	6.9	338	16	US-10-437-963-190096	Sequence 190096, A
44	82.5	6.7	1473	12	US-10-182-822A-8	Sequence 8, Appli
45	82	6.7	450	14	US-10-156-761-7904	Sequence 7904, Ap

ALIGNMENTS

RESULT 1

US-09-931-704-5
; Sequence 5, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Methods and Compositions for Treating IgE-Related Disease Using N
; FILE OF INVENTION: Inhibitors
; FILE REFERENCE: A-695
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Murine
US-09-931-704-5

Query Match 100.0%; Score 1224; DB 9; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.8e-113;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDLRAGDSWGMCLCTVLMHLPAYPALNRTGDPGPGSIQKTYDLTRYLHOLSLAGT	60
Db	1	MDLRAGDSWGMCLCTVLMHLPAYPALNRTGDPGPGSIQKTYDLTRYLHOLSLAGT	60
Qy	61	YLNLYGPPNEPDPNPPRRLGAETLPRATVNLVWRSNDRLRLTQNYEAYSHLLCYRL	120
Db	61	YLNLYGPPNEPDPNPPRRLGAETLPRATVNLVWRSNDRLRLTQNYEAYSHLLCYRL	120
Qy	121	NRQAATAELRRSLAHFCTSLQGLLSIAGWMATLYGPIPOPLPGTEPAWAPGPAHSDFLQ	180
Db	121	NRQAATAELRRSLAHFCTSLQGLLSIAGWMATLYGPIPOPLPGTEPAWAPGPAHSDFLQ	180
Qy	181	KMDDFWLLKELQTLWRSKDFNRLKKMQPPAASVTLLEAHGF	225

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Db 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAASVTLHLEAHGF 225
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US-09-931-704-2
RESULT 2
US-09-931-704-2
; Sequence 2, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Methods and Compositions for Treating IgE-Related Disease Using N
; FILE OF INVENTION: Inhibitors
; FILE REFERENCE: A-695
; CURRENT APPLICATION NUMBER: US/09/931,704
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-931-704-2

Query Match 97.5%; Score 1193; DB 9; Length 225;
Best Local Similarity 96.9%; Pred. No. 3.4e-110;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMCLACTVWLWHPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
DB 1 MDLRAGDSWGMCLACTVWLWHPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
QY 61 YLNYLGPPFNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
DB 61 YLNYLGPPFNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
QY 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
DB 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
QY 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAASVTLHLEAHGF 225
DB 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAASVTLHLEAHGF 225

US-10-212-793-2
Query Match 97.5%; Score 1193; DB 14; Length 225;
Best Local Similarity 96.9%; Pred. No. 3.4e-110;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMCLACTVWLWHPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
DB 1 MDLRAGDSWGMCLACTVWLWHPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
QY 61 YLNYLGPPFNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
DB 61 YLNYLGPPFNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
QY 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
DB 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
QY 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAASVTLHLEAHGF 225
DB 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAASVTLHLEAHGF 225

US-10-408-765A-785
RESULT 4
US-10-408-765A-785
; Sequence 785, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 785
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-785

Query Match 97.5%; Score 1193; DB 16; Length 225;
Best Local Similarity 96.9%; Pred. No. 3.4e-110;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMCLACTVWLWHPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
DB 1 MDLRAGDSWGMCLACTVWLWHPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
QY 61 YLNYLGPPFNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
DB 61 YLNYLGPPFNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
QY 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
DB 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
QY 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAASVTLHLEAHGF 225
DB 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAASVTLHLEAHGF 225

US-10-212-793-2
RESULT 3
US-10-212-793-2
; Sequence 2, Application US/10212793
; Publication No. US20030087395A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Cardiostrophin-Like Cytokine
; FILE REFERENCE: PF385D1C1
; CURRENT APPLICATION NUMBER: US/10/212,793
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 09/438,299
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/106,182
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: US 60/051,311
; PRIOR FILING DATE: 1997-06-30
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 2
; LENGTH: 225
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: signal
; LOCATION: (-27)..(-1)
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(198)
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US-10-212-793-2
Query Match 97.5%; Score 1193; DB 14; Length 225;
Best Local Similarity 96.9%; Pred. No. 3.4e-110;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMCLACTVWLWHPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
DB 1 MDLRAGDSWGMCLACTVWLWHPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
QY 61 YLNYLGPPFNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
DB 61 YLNYLGPPFNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
QY 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
DB 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
QY 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAASVTLHLEAHGF 225
DB 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAASVTLHLEAHGF 225

US-10-408-765A-785
RESULT 4
US-10-408-765A-785
; Sequence 785, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 785
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-785

Query Match 97.5%; Score 1193; DB 16; Length 225;
Best Local Similarity 96.9%; Pred. No. 3.4e-110;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMCLACTVWLWHPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
DB 1 MDLRAGDSWGMCLACTVWLWHPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
QY 61 YLNYLGPPFNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
DB 61 YLNYLGPPFNEPDPNPRGAEATLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGL 120
QY 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
DB 121 NRQAATAELRRSLAHFCTSLQGLLSIAGVMAATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
QY 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAASVTLHLEAHGF 225
DB 181 KMDDFWLLKELQTLWLRSAKDFNRLKKMKQPPAAASVTLHLEAHGF 225

US-10-212-793-2
RESULT 3
US-10-212-793-2
; Sequence 2, Application US/10212793
; Publication No. US20030087395A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Cardiostrophin-Like Cytokine
; FILE REFERENCE: PF385D1C1
; CURRENT APPLICATION NUMBER: US/10/212,793
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 09/438,299
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/106,182
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: US 60/051,311
; PRIOR FILING DATE: 1997-06-30
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 2
; LENGTH: 225
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: signal
; LOCATION: (-27)..(-1)
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(198)
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; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1346
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1346

Query Match 97.5%; Score 1193; DB 12; Length 253;
Best Local Similarity 96.9%; Pred. No. 4e-110;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGLACLTWHLPAVPAALNRTPGPGPSIQKTYDLTRYLEHQRLSLAGT 60
DB 29 MDLRAGDSWGLACLTWHLPAVPAALNRTPGPGPSIQKTYDLTRYLEHQRLSLAGT 88
QY 61 YLNYLGPPFNPFPNPPRLGAETLPRAVTNLEWVRSNDRLRLTQNYEAYSHLLCYLRGL 120
DB 89 YLNYLGPPFNPFPNPPRLGAETLPRAVTNLEWVRSNDRLRLTQNYEAYSHLLCYLRGL 148
QY 121 NROATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLGTEPTWTGPAHSDFLQ 180
DB 149 NROATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLGTEPTWTGPAHSDFLQ 208
QY 181 KMDDFWLLKELQTLWRSKADFNRLKKKMQPPAAASVTLLHLEAHGF 225
DB 209 KMDDFWLLKELQTLWRSKADFNRLKKKMQPPAAAVTLHLGAHGF 253

RESULT 6
US-10-276-774-2266
; Sequence 2266, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2266
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2266

Query Match 95.7%; Score 1171; DB 12; Length 321;
Best Local Similarity 96.0%; Pred. No. 8.4e-108;
Matches 214; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 LRAGDSWGLACLTWHLPAVPAALNRTPGPGPSIQKTYDLTRYLEHQRLSLAGTYL 62
DB 99 LPTGDSWGLACLTWHLPAVPAALNRTPGPGPSIQKTYDLTRYLEHQRLSLAGTYL 158
QY 63 NYLGPPFNPFPNPPRLGAETLPRAVTNLEWVRSNDRLRLTQNYEAYSHLLCYLRGLNR 122
DB 159 NYLGPPFNPFPNPPRLGAETLPRAVTNLEWVRSNDRLRLTQNYEAYSHLLCYLRGLNR 218
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QY 123 QAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLGTEPTWTGPAHSDFLQXM 182
DB 219 QAATAELRSLAHFCTSLQGLLSIAGVMAALGYPLPQPLGTEPTWTGPAHSDFLQXM 278
QY 183 DDFWLLKELQTLWRSKADFNRLKKKMQPPAAASVTLLHLEAHGF 225
DB 279 DDFWLLKELQTLWRSKADFNRLKKKMQPPAAAVTLHLGAHGF 321

RESULT 7
US-09-864-761-40014
; Sequence 40014, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40014
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005849.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
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us-09-931-704-5.rapb

Tue Aug 17 06:05:03 2004

TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

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; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EST HUMAN HIT: A1752561.1, EVALUAE 3.00e-66
; OTHER INFORMATION: SWISSPROT HIT: Q63086, EVALUAE 8.00e-03
US-09-864-761-40014

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WOOD, WILLIAM
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/107,931
FILING DATE: 26-Mar-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/364,187
FILING DATE: 30-Jul-1999
APPLICATION NUMBER: 08/286,304
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 894P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-107-931-3

Query Match 9.0%; Score 110.5; DB 14; Length 203;
Best Local Similarity 27.4%; Pred. No. 0.013;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;
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Db 84 -SERLR--QDAALSVLPALLDAVRRQAEINPRAPRLRSLEDAARQVRAALGAAYETVL 140
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Db 141 AALGAAARG--PGPEPVTATLFTANSTAGIFS AKVILGFHVCGLYGEWVSRTGDLGQL 197

RESULT 11
US-10-407-303-3
Sequence 3, Application US/10407303
Publication No. US20040006018A1
GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Methods of Stimulating the Proliferation and
TITLE OF INVENTION: Differentiation of Satellite Cells Into Myoblasts by
TITLE OF INVENTION: Contact with CT-1
FILE REFERENCE: P0994R1D2C1
CURRENT APPLICATION NUMBER: US/10/407,303
CURRENT FILING DATE: 2003-04-03
PRIORITY APPLICATION NUMBER: US 09/724,772
PRIORITY FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: US 08/797,014
PRIOR FILING DATE: 1997-02-07
PRIOR APPLICATION NUMBER: US 60/049,998
PRIOR FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 3
LENGTH: 203
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: Amino Acid
LOCATION: Full
OTHER INFORMATION:
US-10-407-303-3
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Best Local Similarity 27.4%; Pred. No. 0.013;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;
QY 40 IQKTYDLTRYLEHQRLSLAGTYLVNLYGPPFNEPDPNPRLL---GAETLPRATVNLVWRS 96
Db 27 IRQTHNLARLLTKYAEQLLEEVVQQQGEFGLPGFSPRLPLAGLSGAPSHAGLPV--- 83
QY 97 LNDRLRLTONYEAYSHLLCYLRGLNRQAA-----TAE LRSLAHFCTSLQGLIGSIAGVM 151
Db 84 -SERLR--QDAALSVLPALLDAVRRQAEINPRAPRLRSLEDAARQVRAALGAAYETVL 140
QY 152 ATLGYPPLPQPLPGTEPA-----WAPGPAHSDFLQKMDDFWLLKELQTLWLRSAKDNRL 205
Db 141 AALGAAARG--PGPEPVTATLFTANSTAGIFS AKVILGFHVCGLYGEWVSRTGDLGQL 197

RESULT 12
US-10-722-095-3
Sequence 3, Application US/10722095
Publication No. US20040116678A1
GENERAL INFORMATION:
APPLICANT: Baker, Jeffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
FILE REFERENCE: P0894P1D2C6
CURRENT APPLICATION NUMBER: US/10/722,095
CURRENT FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: US 09/896,856
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/033,114
PRIOR FILING DATE: 1998-03-02
PRIOR APPLICATION NUMBER: US 08/733,850
PRIOR FILING DATE: 1996-10-18
PRIOR APPLICATION NUMBER: US 08/443,129
PRIOR FILING DATE: 1995-05-17
PRIOR APPLICATION NUMBER: US 08/286,304
PRIOR FILING DATE: 1994-08-05
PRIOR APPLICATION NUMBER: US 08/233,609
PRIOR FILING DATE: 1994-04-25
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 3
LENGTH: 203
TYPE: PRT
ORGANISM: Mus Musculus
US-10-722-095-3

Query Match 9.0%; Score 110.5; DB 16; Length 203;
Best Local Similarity 27.4%; Pred. No. 0.013;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;
QY 40 IQKTYDLTRYLEHQRLSLAGTYLVNLYGPPFNEPDPNPRLL---GAETLPRATVNLVWRS 96
Db 27 IRQTHNLARLLTKYAEQLLEEVVQQQGEFGLPGFSPRLPLAGLSGAPSHAGLPV--- 83

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DB      141 AALGAARAG--PGPEPVATVLTFTANSTAGIFSARVLGHFVGVGHWKSGIEDLQJL 197
RESULT 13
US-10-282-122A-69553
; Sequence 69553, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69553
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Pseudomonas syringae
US-10-282-122A-69553
Query March      9.8%; Score 109; DB 12; Length 471;
Best Local Similarity 25.5%; Pred. No. 0.053; 100% Identity 100%

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[illegible]

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 06:43:28 ; Search time 15 Seconds
(without alignments)
774.390 Million cell updates/sec

Title: US-09-931-704-5

Perfect score: 1224

Sequence: 1 MDLRAGDSWGMACLTCTVLW.....KKXQPPAASVTLELRHGF 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listed first 45 summaries

Database : Issued Patents AA.*

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- 2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
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- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1224	100.0	225	1	US-08-792-019B-5
2	1224	100.0	225	3	US-08-988-819-5
3	1224	100.0	225	3	US-09-016-534-5
4	1193	97.5	225	1	US-08-792-019B-2
5	1193	97.5	225	3	US-08-106-182-2
6	1193	97.5	225	3	US-08-988-819-2
7	1193	97.5	225	3	US-09-016-534-2
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12	110.5	9.0	203	1	US-08-442-745-3
13	110.5	9.0	203	1	US-08-443-129-3
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18	91.5	7.5	201	1	US-08-444-083-8
19	91.5	7.5	201	1	US-08-286-304-8
20	91.5	7.5	201	1	US-08-442-745-8
21	91.5	7.5	201	1	US-08-443-129-8
22	91.5	7.5	201	1	US-08-443-952-8
23	91.5	7.5	201	1	US-08-443-130-8
24	91.5	7.5	201	1	US-08-792-019B-11
25	91.5	7.5	201	3	US-08-106-182-4
26	91.5	7.5	201	3	US-08-988-819-11
27	91.5	7.5	201	3	US-08-988-911-8

28 91.5 7.5 201 3 US-09-016-534-11 Sequence 11, Appl
29 91.5 7.5 201 4 US-09-648-183-3 Sequence 3, Appl
30 91.5 7.5 201 5 PCT-US95-04467-8 Sequence 8, Appl
31 90 7.4 195 1 US-07-959-284-5 Sequence 5, Appl
32 90 7.4 195 2 US-08-308-736A-5 Sequence 5, Appl
33 90 7.4 195 4 US-08-645-107A-5 Sequence 5, Appl
34 90 7.4 195 4 US-09-197-349-5 Sequence 5, Appl
35 90 7.4 195 4 US-09-031-693-5 Sequence 5, Appl
36 90 7.4 195 4 US-09-454-380-5 Sequence 5, Appl
37 90 7.4 195 5 PCT-US92-08258-2 Sequence 2, Appl
38 90 7.4 195 5 PCT-US93-09649A-5 Sequence 5, Appl
39 90 7.4 195 5 PCT-US93-09649-5 Sequence 5, Appl
40 89 7.3 737 4 US-09-252-991A-22539 Sequence 22539, A
41 87.5 7.1 426 4 US-09-252-991A-29288 Sequence 29288, A
42 85.5 7.0 560 2 US-08-756-317-11 Sequence 11, Appl
43 85.5 7.0 8991 4 US-08-714-741-32 Sequence 32, Appl
44 83 6.8 760 4 US-09-252-991A-18711 Sequence 18711, A
45 82.5 6.7 2628 3 US-09-413-814-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-792-019B-5
; Sequence 5, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,019B
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-792-019B-5

Query Match 100.0%; Score 1224; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1e-122;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACLTCTVLWHPALNRTGDPGPGPSIQKTYDLTRYLEHQLSLAGT 60
DB 1 MDLRAGDSWGMACLTCTVLWHPALNRTGDPGPGPSIQKTYDLTRYLEHQLSLAGT 60
QY 61 YLNYLGPPNEDFPNPRLGATLPRATVNVWLSLNDRLRLTONYEAYSHLLCYLRGL 120
DB 61 YLNYLGPPNEDFPNPRLGATLPRATVNVWLSLNDRLRLTONYEAYSHLLCYLRGL 120
QY 121 NROAATAELRRSLAHFCTSLQGLLSIAGVMATLGHPLPQPLPGTEPAWAPGPAHSDFLQ 180

Db 121 NROQATAELRRSLAHFCTSLQGLLSIAGVMATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
QY 181 KMDDFWLLKELOTWLRSAKDFNRLKKKQPPAASVTLHLEAHGF 225
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RESULT 2

US-08-988-819-5
; Sequence 5, Application US/08988819
; Patent No. 6054294
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,819
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-988-819-5

Query Match 100.0%; Score 1224; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 1e-122;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACLTCTVLMHLPVAPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
Db 1 MDLRAGDSWGMACLTCTVLMHLPVAPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
QY 61 YLYLGPFPNEPDNPPRIGATLPRATVNLVWRSINDRRLTQNYEAYSHLLCYLRGL 120
Db 61 YLYLGPFPNEPDNPPRIGATLPRATVNLVWRSINDRRLTQNYEAYSHLLCYLRGL 120
QY 121 NROQATAELRRSLAHFCTSLQGLLSIAGVMATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
Db 121 NROQATAELRRSLAHFCTSLQGLLSIAGVMATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
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Db 181 KMDDFWLLKELOTWLRSAKDFNRLKKKQPPAASVTLHLEAHGF 225

RESULT 3

US-09-016-534-5
; Sequence 5, Application US/09016534
; Patent No. 6143874
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI

; APPLICANT: ELLIOTT, GARY S.
; APPLICANT: SARMIENTO, ULLA
; APPLICANT: SENALDI, GIORGIO
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,534
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442B
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-534-5

Query Match 100.0%; Score 1224; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 1e-122;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACLTCTVLMHLPVAPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
Db 1 MDLRAGDSWGMACLTCTVLMHLPVAPALNRTGDPGPGPSIQKTYDLTRYLHQLRSLAGT 60
QY 61 YLYLGPFPNEPDNPPRIGATLPRATVNLVWRSINDRRLTQNYEAYSHLLCYLRGL 120
Db 61 YLYLGPFPNEPDNPPRIGATLPRATVNLVWRSINDRRLTQNYEAYSHLLCYLRGL 120
QY 121 NROQATAELRRSLAHFCTSLQGLLSIAGVMATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
Db 121 NROQATAELRRSLAHFCTSLQGLLSIAGVMATLGYPLPQPLPGTEPAWAPGPAHSDFLQ 180
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Db 181 KMDDFWLLKELOTWLRSAKDFNRLKKKQPPAASVTLHLEAHGF 225

RESULT 4

US-08-792-019B-2
; Sequence 2, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:


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; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,304
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/233609
; FILING DATE: 25-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 894PI
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-286-304-3

Query Match          9.0%; Score 110.5; DB 1; Length 203;
Best Local Similarity 27.4%; Pred. No. 0.00081;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

QY 40 IKTQYDLTRYLEHQLRSLAGTYLNYLGGPPNPPNPPRL---GAETLPRTATVNLVWRS 96
Db 27 IRTQHNLRLLTKYAEQLLEEVYQQQGEFFGLPGFSPPLPLAGLGGPAPSHAGLPV--- 83
QY 97 LNDRLRLTQNYEAYSHLLCYLRGLNRQAA-----TAEIERSLAHFTCSLOGLLGSIAGVM 151
Db 84 -SERLR--QDAALSVLPAALLDAVRRRQAEINPRAPRLRLSLSDAARQVRALGAAVETVL 140
QY 152 ATLGLYPLPQLPQTEPA-----WAPGPAHSDFLQKMDDFWLLKELQTLWLRSAKDFNRL 205
Db 141 AALGAARG--PGPEPVTVATLTANSTAGIFSARKVLGHVCGLYGEWVSRTGDLGQL 197

RESULT 12
US-08-442-745-3
; Sequence 3, Application US/08442745
; Patent No. 5624806
; GENERAL INFORMATION:
; APPLICANT: Baker, Joffe
; APPLICANT: Chien, Kenneth
; APPLICANT: King, Kathleen
; APPLICANT: Pennica, Diane
; APPLICANT: Wood, William
; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,745
; FILING DATE: 17-may-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/233609
```

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; FILING DATE: 25-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286304
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: 894PID1
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-442-745-3

Query Match          9.0%; Score 110.5; DB 1; Length 203;
Best Local Similarity 27.4%; Pred. No. 0.00081;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

QY 40 IKTQYDLTRYLEHQLRSLAGTYLNYLGGPPNPPNPPRL---GAETLPRTATVNLVWRS 96
Db 27 IRTQHNLRLLTKYAEQLLEEVYQQQGEFFGLPGFSPPLPLAGLGGPAPSHAGLPV--- 83
QY 97 LNDRLRLTQNYEAYSHLLCYLRGLNRQAA-----TAEIERSLAHFTCSLOGLLGSIAGVM 151
Db 84 -SERLR--QDAALSVLPAALLDAVRRRQAEINPRAPRLRLSLSDAARQVRALGAAVETVL 140
QY 152 ATLGLYPLPQLPQTEPA-----WAPGPAHSDFLQKMDDFWLLKELQTLWLRSAKDFNRL 205
Db 141 AALGAARG--PGPEPVTVATLTANSTAGIFSARKVLGHVCGLYGEWVSRTGDLGQL 197

RESULT 13
US-08-443-129-3
; Sequence 3, Application US/08443129
; Patent No. 5627073
; GENERAL INFORMATION:
; APPLICANT: Baker, Joffe
; APPLICANT: Chien, Kenneth
; APPLICANT: King, Kathleen
; APPLICANT: Pennica, Diane
; APPLICANT: Wood, William
; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,129
; FILING DATE: 17-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/233609
; FILING DATE: 25-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: 894PID1
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-442-745-3
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